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OM protein - protein search, using sw model

Run on: August 12, 2005, 15:00:58 ; Search time 73 Seconds

(without alignments)  
328.481 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_105\_166

Perfect score: 315

Sequence: 1 ENKLSPVNLPELRRQSG.....SPALPGLKSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1980s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	100.0	166	2	AAW75785 Human lym
2	315	100.0	166	5	AAE15494 Human TAC
3	315	100.0	246	6	ABP97720 Amino aci
4	315	100.0	246	8	ADK00762 Native hu
5	315	100.0	247	3	ASY93998 Human BR4
6	315	100.0	247	7	ABR61797 Human RYZ
7	315	100.0	265	4	AAE09244 Human TAC
8	315	100.0	266	6	ABP97723 Amino aci
9	315	100.0	293	3	AAW75783 Human lym
10	315	100.0	293	3	AAAB36312 Human neu
11	315	100.0	293	3	AAAY94000 A transme
12	315	100.0	293	4	AAE09240 Human TAC
13	315	100.0	293	4	AAV71914 Human tum
14	315	100.0	293	5	AAO14130 Human tra
15	315	100.0	293	5	ABB81488 Human TAC
16	315	100.0	293	5	AAU99512 Human TAC
17	315	100.0	293	5	AAE28962 Human TAC
18	315	100.0	293	5	AAU75408 Tumour ne
19	315	100.0	293	5	AAU09900 Human AGP
20	315	100.0	293	5	AAE15493 Human tra
21	315	100.0	293	5	ABG71496 Human tum
22	315	100.0	293	6	AAE35211 Human TAC
23	315	100.0	293	6	ABP60551 Human tum
24	315	100.0	293	6	ABP97716 Amino aci
25	315	100.0	293	6	AAO29592 Human DIT

#### ALIGNMENTS

RESULT 1

AAW75785  
ID AAW75785 standard; protein; 166 AA.

XX  
AC AAW75785;

XX  
DT 18-JAN-1999 (first entry)

XX  
DE Human lymphocyte surface receptor extracellular domain.

XX  
KW TAC1; transmembrane activator and CAML-interactor;

XX  
KW calcium signal-modulating cyclophilin ligand; human;

XX  
KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;

XX  
KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;

XX  
KW immunosuppressive; graft versus host disease; transplant rejection;

XX  
KW therapy; signal transduction.

XX  
OS Homo sapiens.

XX  
PN WO9839361-A1.

XX  
PD 11-SEP-1998.

XX  
PF 03-MAR-1998; 98WO-US004270.

XX  
PR 03-MAR-1997; 97US-00810572.

XX  
PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX  
PI Bram RJ, Von Bulow G;

XX  
PI MPI; 1998-506346/43.

XX  
DR N-PSDB; AAV57330.

XX  
XX New isolated transmembrane activator protein - used to develop products

XX  
XX for treating e.g. infections, cancers, autoimmune and inflammatory

XX  
XX conditions, transplant rejection or graft-versus-host disease.

XX  
XX Claim 8; Page 73; 89pp; English.

XX  
XX This is the amino acid sequence of the N-terminal, i.e. the

XX  
XX extracellular, domain of novel human transmembrane activator and CAML-

XX  
XX interactor (TAC1) protein (see AAW75783). TAC1 is a lymphocyte receptor

XX  
XX protein that is involved in the calcium activation pathway. It is

XX  
XX normally present in B-lymphocytes, and to a much lesser extent in

XX  
XX immature T-lymphocytes, and can therefore be targeted to specifically

XX  
XX regulate B cell responses without affecting T cell activity. The

XX  
XX extracellular domain of TAC1 functions as a binding site for a ligand

26	315	100.0	293	7	ADF72628	Adf72628 Human tum
27	315	100.0	293	7	ABF77379	Abf77379 Human tum
28	315	100.0	293	7	ABM85745	Abm85745 Human pro
29	315	100.0	293	8	ADK00754	Adk00754 Native hu
30	315	100.0	293	8	ADJ92514	Adj92514 Human TAC
31	315	100.0	293	8	ADN03174	Adn03174 Human TAC
32	315	100.0	293	8	ADQ76815	Adq76815 Human TAC
33	315	100.0	293	8	ADQ94440	Adq94440 Neutrokin
34	315	100.0	294	8	ADK00765	Adk00765 hTAC1 spl
35	315	100.0	312	5	AAO14135	Aao14135 Protein o
36	310	98.4	397	5	AAE15498	Aae15498 Human TAC
37	300.5	95.4	291	5	AAU10949	Aau10949 Human AGP
38	287	91.1	404	5	AAO14136	Aao14136 Protein o
39	279.5	88.7	57	5	AAU10953	Aau10953 Human AGP
40	260	82.5	392	6	AAE35223	Aae35223 Human TAC
41	141.5	44.9	249	3	AAV94006	Aay94006 A murine
42	141.5	44.9	249	7	ABM85744	Abm85744 Mouse pro
43	85	27.0	357	6	AAE35226	Aae35226 Human TAC
44	84.5	26.8	702	4	ABB63821	Abb63821 Drosophill
45	66	21.0	428	7	ABO75685	AbO75685 Pseudomon

CC that stimulates the activation of the cell by inducing the binding of the  
 CC C-terminal portion (see AAW5784) of TACI to the N-terminal domain of  
 CC CAML. A recombinant form of the extracellular portion of TACI acts as a  
 CC dominant-negative or blocking agent and acts to suppress the immune  
 CC system. It can be used to treat or prevent autoimmune disease, graft  
 CC rejection or graft versus host disease. The extracellular region is also  
 CC used in a claimed method for identifying a ligand for TACI, in which  
 CC binding of a candidate molecule is determined by detecting cellular  
 CC activation of the AP-1, CAMP or NF-KB pathway, of NF-AT transcription  
 CC factor, or of NF-AT dependent transcription  
 XX

SQ Sequence 166 AA;

Query Match 100.0%; Score 315; DB 2; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGEVNNDSNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 105 ENKLSPVNLPPELRRQSRGEVNNDSNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 QY 61 ST 62  
 DB 165 ST 166

\*RESULT 2

AAEL5494  
 ID AAE15494 standard; protein; 166 AA.

AC AAE15494;

DT 12-MAR-2002 (first entry)

XX Human TACI extracellular domain.

XX Human; transmembrane activator and intracellular CAML interactor; TACI;  
 KW cytosolic; B cell maturation protein; BCMA; tumour necrosis factor; TNF;  
 KW lymphoproliferative disorder; tumour; lung; gastrointestinal; pancreatic;  
 KW prostate; inflammation; immune disorder; diarrhoea; psoriasis; colitis;  
 KW drug allergy; dermatitis; pneumonia; asthma; inflammatory bowel disease;  
 KW Crohn's disease; scleroderma; autoimmune disease; multiple sclerosis;  
 KW human immunodeficiency virus; HIV; systemic lupus erythematosus; cancer;  
 KW rheumatoid arthritis; atherosclerosis.

XX Homo sapiens.

XX WO200187979-A2.

XX 22-NOV-2001.

XX 14-MAY-2001; 2001WO-US015567.

XX 12-MAY-2000; 2000US-0204039P.

XX 27-JUN-2000; 2000US-0214591P.

XX 14-MAY-2001; 2001US-00214591.

XX (AMGE-) AMGEN INC.

XX Theill LE, Yu G;

XX WPI; 2002-066686/09.

XX Inhibiting activity of B cell maturation protein and/or transmembrane  
 PT activator and intracellular cyclophilin ligand interactor, by  
 PT administering a binding partner for APRIL, a tumor necrosis factor family  
 PT ligand.

XX Claim 1; Fig 12A; 94pp; English.

XX The invention relates to a method for inhibiting TACI (transmembrane  
 CC activator and intracellular CAML interactor) and/or B cell maturation  
 CC protein (BCMA) activity in a mammal. The method comprises administering a

CC specific binding partner for APRIL (G70, a tumour necrosis factor-TNF  
 CC family ligand), having the consensus region of TACI, BCMA, or the TACI/  
 CC BCMA extracellular consensus sequence, but not the extracellular region  
 CC of TACI or BCMA. The method is useful for inhibiting activity of TACI  
 CC and/or BCMA in a mammal which is useful for treating B-cell or T-cell  
 CC lymphoproliferative disorders, one or more solid tumours such as lung,  
 CC gastrointestinal, pancreatic or prostate tumour. APRIL, BCMA and TACI  
 CC antagonists are useful for treating inflammation and immune function  
 CC diseases such as diarrhoea, psoriasis, allergies, pneumonia, atopic  
 CC dermatitis, respiratory allergic disease (asthma, hypersensitivity lung  
 CC disease), drug and insect sting allergy, inflammatory bowel disease  
 CC (Crohn's disease, colitis), scleroderma, autoimmune disease (multiple  
 CC sclerosis, rheumatoid arthritis, systemic lupus erythematosus), fungal,  
 CC bacterial, protozoal and viral infections (HIV), atherosclerosis, cancer  
 CC with leucocyte infiltration of the skin or organs. The present sequence  
 CC is human TACI protein extracellular domain  
 XX

SQ Sequence 166 AA;

Query Match 100.0%; Score 315; DB 5; Length 166;  
 Best Local Similarity 100.0%; Pred. No. 5.1e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGEVNNDSNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 105 ENKLSPVNLPPELRRQSRGEVNNDSNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 QY 61 ST 62  
 DB 165 ST 166

RESULT 3

ABP97720  
 ID ABP97720 standard; protein; 246 AA.

XX ABP97720;

XX 28-MAY-2003 (first entry)

XX Amino acid sequence of human TACI receptor.

XX Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
 KW TALL-1; April; systemic lupus erythematosus.

XX Homo sapiens.

XX WO2003014294-A2.

XX 20-FEB-2003.

XX 24-JUL-2002; 2002WO-US023487.

XX 03-AUG-2001; 2001US-0310114P.

XX 30-APR-2002; 2002US-0377171P.

XX (GETH ) GENENTECH INC.

XX Dixit V, Grewal I, Ridgway J, Yan M;

XX WPI; 2003-256560/25.

XX N-PSDB; ABZ68874.

XX New nucleic acid encoding a TACIs or BR3 polypeptide, useful for

XX preparing a composition for treating systemic lupus erythematosus.

XX Disclosure; Fig 5B; 153pp; English.

XX The present sequence represents a human TACI polypeptide. The  
 CC specification also describes BR3 polypeptides. TACI and BR3 are  
 CC receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and April  
 CC bind to the TACI receptor, while TNF family ligands TALL-1 also binds to  
 CC BR3 receptor. The TACI and BR3 receptor nucleic acid is useful for

CC preparing a composition for treating systemic lupus erythematosus

XX Sequence 246 AA;

Query Match 100.0%; Score 315; DB 6; Length 246;

Best Local Similarity 100.0%; Pred. No. 8.5e-33; Mismatches 0; Indels 0; Gaps 0;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYOGLHGRGSEASPALPGLKLSADQVALVY 60

DB 59 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYOGLHGRGSEASPALPGLKLSADQVALVY 118

QY 61 ST 62

DB 119 ST 120

RESULT 4

ADK00762

ID ADK00762 standard; protein; 246 AA.

XX AC ADK00762;

DT 06-MAY-2004 (first entry)

XX DE Native human TACIs.

XX KW CAML interactor receptor; TACI; Cytostatic; Antiinflammatory;

KW Dermatological; Immunosuppressive; Antirheumatic; Antiarthritic;

KW Antidiabetic; Neuroprotective; Antiasthmatic; Antiallergic; Anti-HIV;

KW Antibacterial; antiparasitic; systemic lupus erythematosus;

KW diabetes mellitus; AIDS.

XX OS Homo sapiens.

XX PN WO2004011611-A2.

XX PD 05-FEB-2004.

XX PF 25-JUL-2003; 2003WO-US023421.

XX PR 25-JUL-2002; 2002US-0398530P.

XX PA (GETH ) GENENTECH INC.

XX PI Chuntharpai A, Grewal I, Kim KJ, Yan M;

XX WPI; 2004-143841/14.

XX DR N-PSDB; ADK00761.

XX New anti-TACI receptor monoclonal antibody, useful for diagnosing and treating pathological conditions associated with tumor necrosis factor, e.g. cancer or immune-related disease, such as rheumatoid arthritis or psoriasis.

XX PS Disclosure; SEQ ID NO 14; 110pp; English.

XX The present invention relates to an isolated monoclonal antibody which binds to a transmembrane activator of and CAML interactor (TACI) receptor. The TACI antibodies are useful for modulating TALL-1 or TACI polypeptide biological activity in mammalian cells, or for diagnosing and treating pathological conditions associated with TNF and TNF receptor-related molecules, e.g. cancer or immune-related disease, such as systemic lupus erythematosus, rheumatoid arthritis, Sjogren's syndrome, systemic vasculitis, diabetes mellitus, Crohn's disease, glomerulonephritis, multiple sclerosis, psoriasis, asthma, urticaria or infectious diseases including AIDS, hepatitis infection, bacterial infection, fungal infection, protozoal infection and parasitic infection. The present sequence represents native human TACIs.

XX SQ Sequence 246 AA;

Query Match 100.0%; Score 315; DB 8; Length 246;

Best Local Similarity 100.0%; Pred. No. 8.5e-33; Mismatches 0; Indels 0; Gaps 0;

Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYOGLHGRGSEASPALPGLKLSADQVALVY 60

DB 59 ENKLSPVNLPPELRRQSRGSEVNNDSNGRYOGLHGRGSEASPALPGLKLSADQVALVY 118

QY 61 ST 62

DB 119 ST 120

RESULT 5

AAV93998

ID AAV93998 standard; protein; 247 AA.

XX AC AAV93998;

XX DT 20-OCT-2000 (first entry)

XX DE Human BR43x2, an isoform of the TACI receptor.

XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein; transmembrane activator and CAML-interactor; tumour necrosis factor; TNF; ztnf4 activity; antibody production; autoimmune disease; amyloidosis; systemic lupus erythematosus; myasthenia gravis; multiple sclerosis; rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis; end stage renal failure; glomerulonephritis; vasculitis; nephritis; renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy; immune response; immunosuppression; graft rejection; joint pain; graft versus host disease; inflammation; swelling; anaemia; septic shock; insulin dependent diabetes mellitus; Crohn's disease; hypertension; renal artery stenosis; occlusion; cholesterol; renal emboli.

XX OS Homo sapiens.

XX Key Location/Qualifiers

XX Domain 1..120

XX FT /note= "extracellular domain"

XX FT Region 25..58

XX FT /note= "cysteine-rich pseudo repeat"

XX FT Domain 121..133

XX FT /note= "transmembrane domain"

XX FT Domain 134..247

XX FT /note= "cytoplasmic domain"

XX PN WO2000040716-A2.

XX PD 13-JUL-2000.

XX PF 07-JAN-2000; 2000WO-US000396.

XX PR 07-JAN-1999; 99US-00226533.

XX PA (ZYMO ) ZYMOGENETICS INC.

XX PI Gross JA, Xu W, Madden K, Yee DP;

XX WPI; 2000-452538/39.

XX DR N-PSDB; AAA58556.

XX Inhibiting ztnf4 activity in a mammal, to treat autoimmune diseases, renal disease, graft versus host disease, and inflammation, comprises administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX Claim 62; Page 145; 175pp; English.

XX The present sequence represents a human BR43x2 polypeptide, which is an isoform of the transmembrane activator and CAML-interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF) receptor. The extracellular domains of BR43x2, TACI or BCMA (a related B cell protein) contain a cysteine rich domain, and are used for inhibiting ztnf4 activity. Ztnf4 is a TNF ligand. They may also be used for inhibiting

CC BR43x2, TAC1 or BCMA receptor-ligand engagement associated with activated  
 CC or resting B lymphocytes, effector T-cells, or with antibody production.  
 CC The antibody production is associated with an autoimmune disease selected  
 CC from systemic lupus erythematosus, myasthenia gravis, multiple sclerosis  
 CC and rheumatoid arthritis. The tnfr4 activity and BR43x2, TAC1 or BCMA  
 CC receptor-ligand engagement is associated with asthma, bronchitis,  
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,  
 CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,  
 CC light chain neuropathy, amyloidosis, moderating immune response,  
 CC immunosuppression, graft rejection, graft versus host disease,  
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint  
 CC pain, swelling, anaemia, or septic shock. BR43x2, TAC1, and BCMA  
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to  
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol  
 CC or renal emboli  
 CC  
 SQ Sequence 247 AA;  
 Query Match 100.0%; Score 315; DB 3; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 59 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118  
 QY 61 ST 62  
 DB 119 ST 120  
 RESULT 6  
 ABR61797  
 ID ABR61797 standard; protein; 247 AA.  
 AC ABR61797;  
 DT 12-SEP-2003 (first entry)  
 DE Human RYZN polypeptide.  
 DE RYZN; TNFRSF; tumour necrosis factor receptor; antiarteriosclerotic;  
 KW type III transmembrane protein; antidiabetic; hypotensive; antilipemic;  
 KW human.  
 KW  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..113  
 FT /note= "extracellular domain"  
 FT Domain 114..136  
 FT /note= "transmembrane domain"  
 FT Domain 137..247  
 FT /note= "intracellular domain"  
 XX WO2003045421-A1.  
 XX  
 XX 05-JUN-2003.  
 XX  
 XX 03-OCT-2002; 2002WO-18004581.  
 XX  
 XX 28-NOV-2001; 2001US-0334152P.  
 XX  
 XX (GEST ) GENSET SA.  
 XX  
 XX Djalynas D, Scalia A, Lucas J, Briggs K;  
 XX WPI; 2003-513616/48.  
 DR N-PSDB; ACC84638.  
 XX  
 XX New agonists or antagonists of RYZN activity, useful for increasing or  
 PT reducing body weight, for maintaining weight loss, and for preventing or  
 PT treating an obesity-related disease or disorder, e.g. atherosclerosis or

PT diabetes.  
 XX  
 PS Example; Page 32-33; 37pp; English.  
 XX  
 CC The invention relates to an agonist or antagonist of RYZN activity. RYZN  
 CC is a member of the Tumour Necrosis Factor Receptor Super Family (TNFRSF)  
 CC and is a Type III transmembrane protein. The agonist or antagonist of  
 CC RYZN activity, or compositions comprising them is useful for preventing  
 CC or treating an obesity-related disease or disorder, such as insulin  
 CC resistance, hyperlipidemia, atherosclerosis, diabetes, hypertension,  
 CC syndrome X, and hyperuricemia. These may also be used to increase or  
 CC reduce body weight, or maintain weight loss. The present sequence  
 CC represents the human RYZN polypeptide  
 XX  
 SQ Sequence 247 AA;  
 Query Match 100.0%; Score 315; DB 7; Length 247;  
 Best Local Similarity 100.0%; Pred. No. 8.6e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 59 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118  
 QY 61 ST 62  
 DB 119 ST 120  
 RESULT 7  
 AAE09244  
 ID AAE09244 standard; protein; 265 AA.  
 XX  
 AC AAE09244;  
 XX  
 DT 19-NOV-2001 (first entry)  
 XX  
 DE Human TAC1 splice variant protein.  
 XX  
 KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;  
 KW TAC1; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200160397-A1.  
 XX  
 PD 23-AUG-2001.  
 XX  
 PF 28-NOV-2000; 2000WO-US032378.  
 XX  
 PR 16-FEB-2000; 2000US-0182938P.  
 PR 22-AUG-2000; 2000US-0226986P.  
 XX  
 XX (GETH ) GENENTECH INC.  
 XX  
 XX Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
 PI Yan M;  
 XX  
 XX WPI; 2001-541628/60.  
 DR  
 XX  
 XX Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
 PT activity, for treating autoimmune disorders and cancer, comprises  
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
 PT antagonists.  
 XX  
 XX Example 1; Fig 6; 160pp; English.  
 PS  
 XX  
 CC The invention relates to methods of using one or more agonists or  
 CC antagonists to modulate the activity of the members of TNF (tumour  
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
 CC TAC1 or BCMA. The method is useful for treating pathological conditions  
 or diseases associated with increased TALL-1 and APRIL expression or

CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid  
 CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
 CC present sequence is human TACI splice variant protein

XX SQ Sequence 265 AA;

Query Match 100.0%; Score 315; DB 4; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 9.4e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGVEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 105 ENKLSPVNLPPELRRQSGVEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62

DB 165 ST 166

RESULT 8

ID ABP97723 standard; protein; 266 AA.

XX AC ABP97723;

XX DT 28-MAY-2003 (first entry)

XX DE Amino acid sequence of an alternatively spliced human TACI receptor.

XX KW Human; TACI; BR3; receptor; tumour necrosis factor ligand; TNF ligand;  
 KW TALL-1; April; systemic lupus erythematosus.

XX OS Homo sapiens.

XX PN WO2003014294-A2.

XX PD 20-FEB-2003.

XX PF 24-JUL-2002; 2002WO-US023487.

XX PR 03-AUG-2001; 2001US-0310114P.

XX PR 30-APR-2002; 2002US-0377171P.

XX PA (GETH ) GENENTECH INC.

XX PI Dixit V, Grewal I, Ridgway J, Yan M;

XX DR WPI; 2003-256560/25.

XX PT New nucleic acid encoding a TACIs or BR3 polypeptide, useful for  
 PT preparing a composition for treating systemic lupus erythematosus.

XX FS Disclosure; Fig 8; 153pp; English.

XX CC The present sequence represents an alternatively spliced human TACI  
 CC polypeptide. The specification also describes BR3 polypeptides. TACI and  
 CC BR3 are receptors. Tumour necrosis factor (TNF) family ligands TALL-1 and  
 CC April bind to the TACI receptor, while TNF family ligands TALL-1 also  
 CC binds to BR3 receptor. The TACI and BR3 receptor nucleic acid is useful  
 CC for preparing a composition for treating systemic lupus erythematosus

XX SQ Sequence 266 AA;

Query Match 100.0%; Score 315; DB 6; Length 266;

Best Local Similarity 100.0%; Pred. No. 9.4e-33;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGVEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60

DB 105 ENKLSPVNLPPELRRQSGVEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62  
 DB 165 ST 166

RESULT 9

AAW75783

ID AAW75783 standard; protein; 293 AA.

XX AC AAW75783;

XX DT 18-JAN-1999 (first entry)

XX DE Human lymphocyte surface receptor TACI.

XX KW TACI; transmembrane activator and CAML-interactor;  
 KW calcium signal-modulating cyclophilin ligand; human;  
 KW lymphocyte surface receptor; human; B-cell; B lymphocyte; infection;  
 KW cancer; rheumatoid arthritis; autoimmune disease; glomerulonephritis;  
 KW immunosuppressive; graft versus host disease; transplant rejection;  
 KW therapy.

XX OS Homo sapiens.

XX FH Key

FT Domain Location/Qualifiers  
 FT 1..166 /label= Extracellular\_domain  
 FT /note= "Claim 8"

FT Peptide 34..71

FT /note= "TNFR\_NGFR motif"

FT Domain 167..186

FT /label= Transmembrane\_domain

FT Domain 197..294

FT /label= Cytoplasmic\_domain

FT /note= "Claim 6"

XX WO9839361-A1.

XX PD 11-SEP-1998.

XX PF 03-MAR-1998; 98WO-US004270.

XX PR 03-MAR-1997; 97US-00810572.

XX PA (SJUD-) ST JUDE CHILDREN'S RES HOSPITAL.

XX PI Bram RJ, Von Bulow G;

XX DR WPI; 1998-506346/43.

XX DR N-PSDB; AAV57328.

XX PT New isolated transmembrane activator protein - used to develop products  
 PT for treating e.g. infections, cancers, autoimmune and inflammatory  
 PT conditions, transplant rejection or graft-versus-host disease.

XX PS Claim 20; Fig 2a; 89pp; English.

XX CC This is the amino acid sequence of novel human transmembrane activator  
 CC and CAML-interactor (TACI) protein, a lymphocyte receptor protein that is  
 CC involved in the calcium activation pathway. TACI is normally present in B  
 CC -lymphocytes, and to a much lesser extent in immature T-lymphocytes, and  
 CC can therefore be targeted to specifically regulate B cell responses  
 CC without affecting T cell activity. TACI cDNA (seeAV57328) was isolated  
 CC from a B-lymphocyte cDNA library using a yeast two-hybrid assay. Also  
 CC claimed are the C-terminal (see AAW5784) and N-terminal (see AAW5785)  
 CC fragments of TACI, recombinant DNA constructs, unicellular hosts, and  
 CC antibodies to TACI protein. Methods are claimed for identifying a ligand  
 CC for TACI and for identifying immunosuppressive drugs that selectively  
 CC block the action of B lymphocytes without affecting mature T lymphocytes.  
 CC TACI can be activated to increase immune system activity, e.g. for  
 CC treating infections or cancers. It can be blocked to provide  
 CC immunosuppression, e.g. for treating autoimmune and inflammatory

CC conditions such as immune complex- induced vasculitis,  
 CC glomerulonephritis, haemolytic anaemia, myasthenia gravis, type II  
 CC collagen-induced arthritis, experimental allergic and hyperacute  
 CC xenograft rejection, rheumatoid arthritis, systemic lupus erythematosus,  
 CC transplant rejection, cancer or graft versus host disease  
 XX

SQ Sequence 293 AA;  
 Query Match 100.0%; Score 315; DB 2; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 |||||  
 DB 105 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 |||||

QY 61 ST 62  
 ||  
 DB 165 ST 166

RESULT 10  
 AAB36312  
 ID AAB36312 standard; protein; 293 AA.

XX AC AAB36312;

XX DT 26-FEB-2001 (first entry)

XX DE Human neutrokin-alpha binding protein TR17 SEQ ID NO:2.

XX KW Human; neutrokin-alpha binding protein; NAR protein; TR17; cytostatic;  
 KW immunosuppressive; neutrotropic; neuroprotective; antiviral; antiallergic;  
 KW hepatotropic; antidiabetic; antinflammatory; antilucer; cardiac;  
 KW ophthalmological; gene therapy; immunodeficiency disorder; diagnosis;  
 KW autoimmune disorder.

XX OS Homo sapiens.

XX PN WO200058362-A1.

XX PD 05-OCT-2000.

XX PF 24-MAR-2000; 2000WO-US007966.

XX PR 26-MAR-1999; 99US-0126599P.

XX PR 10-MAR-2000; 2000US-0188208P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Ullrich S, Baker K;

XX DR WPI; 2000-602359/57.

XX DR N-PSDB; AAC64602.

XX PT Nucleic acid encoding a neutrokin-alpha receptor (NAR) such as TR17,  
 PT useful for producing TR17 protein which is used in the treatment and  
 PT diagnosis of autoimmune and immunodeficiency disorders.

XX PS Claim 1; Fig 1; 398pp; English.

XX CC The present sequence represents the human neutrokin-alpha binding (NAR)  
 CC protein designated TR17. TR17 has cytostatic, immunosuppressive,  
 CC neutrotropic, neuroprotective, antiviral, antiallergic, hepatotropic,  
 CC antidiabetic, antinflammatory, antilucer, cardiac and ophthalmological  
 CC activities and can be used in gene therapy. The TR17 protein and  
 CC antibodies are useful for treating and diagnosing immunodeficiency  
 CC disorders and autoimmune disorders. The TR17 polypeptides,  
 CC polynucleotides, antibodies, agonists and/or antagonists are used for  
 CC treating various other diseases defined in the specification and as  
 CC research tools for studying the phenotypic effects that result from  
 CC inhibiting TR17/TR17 ligand interactions on various cell types

SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 3; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
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 DB 105 ENKLRSPVNLPPELRRQRSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 |||||

QY 61 ST 62  
 ||  
 DB 165 ST 166

RESULT 11

AAY94000

ID AAY94000 standard; protein; 293 AA.

XX AC AAY94000;

XX DT 20-OCT-2000 (first entry)

XX DE A transmembrane activator and CAML-interactor (TACI).

XX KW Human; BR43x2; TACI receptor; extracellular domain; BCMA; B cell protein;  
 KW transmembrane activator and CAML-interactor; tumour necrosis factor; TNF;  
 KW znf4 activity; antibody production; autoimmune disease; amyloidosis;  
 KW systemic lupus erythematosus; myasthenia gravis; multiple sclerosis;  
 KW rheumatoid arthritis; asthma; bronchitis; emphysema; pyelonephritis;  
 KW end stage renal failure; glomerulonephritis; vasculitis; nephritis;  
 KW renal neoplasm; multiple myeloma; lymphoma; light chain neuropathy;  
 KW immune response; immunosuppression; graft rejection; joint pain;  
 KW graft versus host disease; inflammation; swelling; anaemia; septic shock;  
 KW insulin dependent diabetes mellitus; Crohn's disease; hypertension;  
 KW renal artery stenosis; occlusion; cholesterol; renal emboli.

XX OS Homo sapiens.

XX PN WO2000040716-A2.

XX PD 13-JUL-2000.

XX PF 07-JAN-2000; 2000WO-US000396.

XX PR 07-JAN-1999; 99US-00226533.

XX PA (ZYMO) ZYMOGENETICS INC.

XX PI Gross JA, Xu W, Madden K, Yee DP;

XX DR WPI; 2000-452538/39.

XX DR N-PSDB; AAA58558.

XX PT Inhibiting znf4 activity in a mammal, to treat autoimmune diseases,  
 PT renal disease, graft versus host disease, and inflammation, comprises  
 PT administering a BR43x2, TACI or BCMA extracellular domain polypeptide.

XX PS Disclosure; Page 149-150; 175pp; English.

XX CC The present sequence represents a human transmembrane activator and CAML-  
 CC interactor (TACI) receptor. TACI is a tumour necrosis factor (TNF)  
 CC receptor. The extracellular domains of BR43x2 (an isoform of TACI), TACI  
 CC or BCMA (a related B cell protein) receptor contain a cysteine rich  
 CC domain, and are used for inhibiting znf4 activity. Znf4 is a TNF  
 CC ligand. They may also be used for inhibiting BR43x2, TACI or BCMA  
 CC receptor-ligand engagement associated with activated or resting B  
 CC lymphocytes, effector T-cells, or with antibody production. The antibody  
 CC production is associated with an autoimmune disease selected from  
 CC systemic lupus erythematosus, myasthenia gravis, multiple sclerosis and  
 CC rheumatoid arthritis. The znf4 activity and BR43x2, TACI or BCMA  
 CC receptor-ligand engagement is associated with asthma, bronchitis,  
 CC emphysema, end stage renal failure, glomerulonephritis, vasculitis,

CC nephritis, pyelonephritis, renal neoplasms, multiple myelomas, lymphomas,  
 CC light chain neuropathy, amyloidosis, moderating immune response,  
 CC immunosuppression, graft rejection, graft versus host disease,  
 CC inflammation, insulin dependent diabetes mellitus, Crohn's disease, joint  
 CC pain, swelling, anaemia, or septic shock. BR43x2, TACI, and BCMA  
 CC polypeptides, fusions, antibodies, agonists or antagonists can be used to  
 CC treat hypertension, renal artery stenosis, or occlusion, and cholesterol  
 CC or renal emboli

XX SQ Sequence 293 AA;  
 Query Match 100.0%; Score 315; DB 3; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 ENKLSPVNLPPELRRQSRGSEVNNDSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 105 ENKLSPVNLPPELRRQSRGSEVNNDSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 QY 61 ST 62  
 DB 165 ST 166

## RESULT 12

AAE09240  
 ID AAE09240 standard; protein; 293 AA.

XX AC AAE09240;  
 DT 19-NOV-2001 (first entry)  
 XX DE Human TACI protein.  
 XX KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor; TNFR;  
 KW TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; psoriasis.

XX OS Homo sapiens.

XX PN WO200160397-A1.

XX PD 23-AUG-2001.

XX PF 28-NOV-2000; 2000WO-US032378.

XX PR 16-FEB-2000; 2000US-0182938P.

XX PR 22-AUG-2000; 2000US-0226986P.

XX PA (GETH ) GENENTECH INC.

XX PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;  
 PI Yan M;

XX DR WPI; 2001-541628/60.

XX DR N-PSDB; AAD15901.

XX PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological  
 PT activity, for treating autoimmune disorders and cancer, comprises  
 PT exposing the cells to TALL-1 or APRIL polypeptide agonists or  
 PT antagonists.

XX PS Example 1; Fig 1; 160pp; English.

XX CC The invention relates to methods of using one or more agonists or  
 CC antagonists to modulate the activity of the members of TNF (tumour  
 CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR) e.g.  
 CC TACI or BCMA. The method is useful for treating pathological conditions  
 CC or diseases associated with increased TALL-1 and APRIL expression or  
 CC activity. TALL-1 and APRIL antagonists are used to block the interaction  
 CC between APRIL and TALL-1 with TACI or BCMA. They are useful for treating  
 CC a mammal suffering from cancer such as leukaemia, lymphoma, myeloma,  
 CC cancers of lung and colon and autoimmune diseases e.g. rheumatoid

CC arthritis, multiple sclerosis, psoriasis and lupus erythematosus. The  
 CC present sequence is human TACI protein  
 XX SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 4; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSRGSEVNNDSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 105 ENKLSPVNLPPELRRQSRGSEVNNDSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 QY 61 ST 62  
 DB 165 ST 166

## RESULT 13

AAV71914

ID AAV71914 standard; protein; 293 AA.

XX AC AAV71914;

XX DT 26-MAR-2001 (first entry)

XX DE Human tumour necrosis factor receptor (TACI) protein.

XX KW Human; transmembrane activator and CAML interactor; TACI;  
 KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;  
 KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;  
 KW neutrokin alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;  
 KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;  
 KW anarthritic; antirheumatic; immunosuppressive; multiple sclerosis;  
 KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;  
 KW cell death; immunoglobulin E-mediated allergic reaction; IgE.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 2. .166

XX FT FT /label= Extracellular domain  
 FT FT /note= "Binds with amino acids 123-285 of extracellular  
 FT FT domain of TACI-L"

XX EN WO200067034-A1.

XX XX 09-NOV-2000.

XX XX 14-APR-2000; 2000WO-US010282.

XX PR 30-APR-1999; 99US-00302863.

XX XX (IMMV ) IMMUNEX CORP.

XX XX Goodwin RG, Din WS;

XX XX WPI; 2001-016005/02.

XX DR N-PSDB; AAD02006.

XX PT Use of new interactions between tumor necrosis factor receptors (TACI)  
 PT and TACI ligands to screen candidate molecules for determining agonist  
 PT and antagonist interactions which are used for treating inflammation.

XX PS Claim 10; Fig 1b; 46pp; English.

XX CC The present sequence is a human tumour necrosis factor receptor (TACI)  
 CC protein. TACI (transmembrane activator and calcium-signal modulating  
 CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokin  
 CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of TACI/TACI-L  
 CC complex is useful for modulating an intracellular signalling cascade  
 CC mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L complex are  
 CC used to inhibit the interaction between TACI and TACI-L for therapeutic



CC purposes to treat tumour and tumour metastasis and to combat various  
 CC autoimmune diseases e.g. multiple sclerosis and diabetes, as well as  
 CC other disorders, such as viral infection, rheumatoid arthritis, graft  
 CC rejection, and immunoglobulin (Ig) E-mediated allergic reactions and  
 CC inflammation. The interaction is used to study cellular processes  
 CC associated with tumour necrosis factor (TNF)-receptors such as immune  
 CC regulation, cell proliferation, cell death and inflammatory responses.  
 CC The interaction between the extracellular region of TACI and TACI-L can  
 CC be used to further develop understanding of which cell types TACI-L acts  
 CC upon  
 XX Sequence 293 AA;  
 SQ

Query Match 100.0%; Score 315; DB 4; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 105 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 QY 61 ST 62  
 DB 165 ST 166

RESULT 14  
 AA014130  
 ID AAO14130 standard; protein; 293 AA.  
 AC AAO14130;  
 XX  
 DT 02-MAY-2002 (first entry)  
 XX  
 DE Human transmembrane activator CAML interactor protein (TACI).  
 XX  
 KW Human transmembrane activator CAML interactor protein; TACI; cytostatic;  
 KW cell proliferation; tumour; vulnery; renal cell cancer; mastocytoma;  
 KW Kaposi's sarcoma; breast; ovarian carcinoma; rectal; throat; melanoma;  
 KW colon; bladder; mammary adenocarcinoma; gastrointestinal; hyperplasia;  
 KW pharyngeal squamous cell; stomach; cellular hyperproliferation; pannus;  
 KW scleroderma; rheumatoid arthritis; scarring; liver; lung fibrosis;  
 KW uterine.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1..114  
 FT /label= Extracellular\_domain  
 XX  
 PN WO200181417-A2.  
 XX  
 PD 01-NOV-2001.  
 XX  
 XX 27-APR-2001; 2001WO-US040626.  
 XX  
 XX 27-APR-2000; 2000US-0199946P.  
 XX  
 PA (BIOJ ) BIOGEN INC.  
 PA (APOT-) APOTEC R & D SA.  
 XX  
 PI Ambrose C, Thompson J, Schneider P, Rennert P;  
 XX  
 DR WPI; 2002-062027/08.  
 DR N-PSDB; AAK98726.  
 XX  
 XX Treating mamal for condition associated with undesired cell  
 XX proliferation e.g., solid tumor or reducing solid tumor size located in  
 XX mammal comprises administering transmembrane activator CAML interactor  
 XX protein reagent.  
 XX  
 XX Claim 8; Fig 1; 42pp; English.

CC This sequence represents the human transmembrane activator CAML  
 CC interactor protein (TACI). The invention relates to treating a mammal for  
 CC a condition associated with undesired cell proliferation (e.g. a solid  
 CC tumour, or reducing the size of a solid tumour located on or in a mammal)  
 CC comprising administering a transmembrane activator CAML interactor  
 CC protein (TACI) reagent. The TACI reagent has cytostatic and vulnerary  
 CC activity. Treating a mammal (e.g. human, cow, horse, dog, mouse, rat or  
 CC cat) for a condition associated with undesired cell proliferation (e.g.  
 CC cancer such as renal cell cancer, Kaposi's sarcoma, breast cancer,  
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma, colon  
 CC cancer, bladder cancer, mastocytoma, lung cancer, mammary adenocarcinoma,  
 CC pharyngeal squamous cell carcinoma, gastrointestinal cancer or stomach  
 CC cancer). The method is also useful for treating cellular  
 CC hyperproliferation (hyperplasia) such as scleroderma, pannus formation in  
 CC rheumatoid arthritis, post-surgical scarring and lung, liver and uterine  
 CC fibrosis. The TACI reagent of the invention can extend mean survival time  
 CC of a mammal by 25% as compared to the mean survival time of a mammal in  
 CC the absence of administering the TACI reagent. The TACI reagent also  
 CC reduces the size of the tumour by 25% or more  
 XX  
 SQ Sequence 293 AA;

Query Match 100.0%; Score 315; DB 5; Length 293;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-32;  
 Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
 DB 105 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
 QY 61 ST 62  
 DB 165 ST 166

RESULT 15  
 ABB81488  
 ID ABB81488 standard; protein; 293 AA.  
 AC ABB81488;  
 XX  
 DT 02-SEP-2002 (first entry)  
 XX  
 DE Human TACI receptor related protein SEQ ID NO:8.  
 XX  
 KW Human; Znf12; tumour necrosis factor receptor; cytostatic;  
 KW immunosuppressive; dermatological; antiinflammatory; antidiabetic;  
 KW neuroprotective; antirheumatic; antiarthritic; antiasthmatic;  
 KW nephrotropic; hypotensive; gene therapy; B lymphocyte; tumour;  
 KW autoimmune disorder; systemic lupus erythematosus; myasthenia gravis;  
 KW multiple sclerosis; insulin dependent diabetes mellitus; asthma;  
 KW rheumatoid arthritis; bronchitis; emphysema; renal disease; lymphoma;  
 KW glomerulonephritis; vasculitis; chronic lymphoid leukaemia; nephritis;  
 KW pyelonephritis; renal neoplasm; multiple myeloma; amyloidosis;  
 KW light chain neuropathy; hypertension; large vessel disease;  
 KW graft-versus host disease; graft rejection; Crohn's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200238766-A2.  
 XX  
 PD 16-MAY-2002.  
 XX  
 XX 05-NOV-2001; 2001WO-US047018.  
 XX  
 XX 07-NOV-2000; 2000US-0245449P.  
 XX 20-DEC-2000; 2000US-0257131P.  
 XX 28-JUN-2001; 2001US-0301715P.  
 XX 29-AUG-2001; 2001US-0315565P.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Gross JA, Xu W, Henne RM, Grant FJ;





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OM protein - protein search, using sw model

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	315	100.0	166	3	US-09-290-333-6
3	315	100.0	166	4	US-09-782-857A-6
4	315	100.0	166	4	US-09-854-864-15
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7	315	100.0	293	4	US-09-782-857A-2
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12	66	21.0	428	4	US-09-252-991A-24431
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14	64	20.3	341	4	US-09-252-991A-18308
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16	62	19.7	635	4	US-09-252-991A-21514
17	62	19.7	806	1	US-07-980-528-2
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19	61	19.4	412	4	US-09-252-991A-30252
20	61	19.4	487	4	US-09-248-796A-19251
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22	60.5	19.2	954	4	US-09-252-991A-32931
23	60	19.0	349	3	US-09-343-011B-1
24	60	19.0	487	4	US-09-252-991A-18581
25	59.5	18.9	203	4	US-09-134-000C-6471
26	59	18.7	242	4	US-09-270-767-43590
27	59	18.7	710	3	US-09-079-812E-2

28	58.5	18.6	214	4	US-09-252-991A-22902	Sequence 22902, A
29	58.5	18.6	261	4	US-09-252-991A-28545	Sequence 28545, A
30	58.5	18.6	453	4	US-09-270-767-44670	Sequence 44670, A
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32	58	18.4	172	4	US-09-902-540-12693	Sequence 12693, A
33	58	18.4	511	4	US-09-198-452A-509	Sequence 509, App
34	58	18.4	511	4	US-09-438-185A-475	Sequence 475, App
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44	57.5	18.3	584	4	US-09-270-767-43419	Sequence 43419, A
45	57.5	18.3	598	4	US-09-902-540-13703	Sequence 13703, A

#### ALIGNMENTS

RESULT 1  
US-08-810-572A-6  
; Sequence 6, Application US/08810572A  
; Patent No. 5969102  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,572A  
; FILING DATE: 28-FEB-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 166 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEetical: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
US-08-810-572A-6

Query Match 100.0%; Score 315; DB 2; Length 166;  
Best Local Similarity 100.0%; Pred. No. 7.7e-34;

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RESULT 3
US-09-782-857A-6
; Sequence 6, Application US/09782857A
; Patent No. 6500428
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE
; THEREOF
;
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,857A
; FILING DATE: 14-Feb-2001
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/810,572
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1340-1-007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
;
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 166 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
;
US-09-782-857A-6

Query Match 100.0%; Score 315; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 7,7e-34;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSFVNLPPELRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 60
DB 105 ENKLRSFVNLPPELRQRSGEVENNSDNGRYQGLEHRGSEASPALPGLKLSADQVALVY 164

QY 61 ST 62
DB 165 ST 166

RESULT 4
US-09-854-864-15
; Sequence 15, Application US/09854864
; Patent No. 6774106
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,

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; TITLE OF INVENTION: BLYS/AGP-3, AND TAC1  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-854-864-15

Query Match 100.0%; Score 315; DB 4; Length 166;  
Best Local Similarity 100.0%; Pred. No. 7.7e-34;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSFVNLPPELRRQSRGSEVNNNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSFVNLPPELRRQSRGSEVNNNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62  
Db 165 ST 166

RESULT 5  
US-08-810-572A-2  
; Sequence 2, Application US/08810572A  
; Patent No. 5969102  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/810,572A  
; FILING DATE: 28-FEB-1997  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007  
; TELEPHONE: 201-487-5900  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 293 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal

; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; US-08-810-572A-2

Query Match 100.0%; Score 315; DB 2; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.6e-33;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 105 ENKLRSFVNLPPELRRQSRGSEVNNNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62  
Db 165 ST 166

RESULT 6  
US-09-290-333-2  
; Sequence 2, Application US/09290333  
; Patent No. 6316222  
; GENERAL INFORMATION:  
; APPLICANT: Bram, Richard J.  
; APPLICANT: von Bulow, Gotz  
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS  
; TITLE OF INVENTION: CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE  
; THEREOF  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/290,333  
; FILING DATE: 12-Apr-1999  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 1340-1-007 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 293 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Homo sapiens  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
; US-09-290-333-2

Query Match 100.0%; Score 315; DB 3; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.6e-33;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSFVNLPPELRRQSRGSEVNNNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSFVNLPPELRRQSRGSEVNNNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164

QY	61 ST 62	
Db	165 ST 166	
<p>RESULT 7</p> <p>US-09-782-857A-2</p> <p>Sequence 2, Application US/09782857A</p> <p>Patent No. 6500428</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Bram, Richard J.</p> <p>von Bulow, Gotz</p> <p>TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS</p> <p>CAML, NUCLEIC ACIDS ENCODING THE SAME AND METHODS OF USE</p> <p>THEREOF</p> <p>NUMBER OF SEQUENCES: 10</p> <p>CORRESPONDENCE ADDRESS:</p> <p>ADDRESSEE: David A. Jackson, Esq.</p> <p>STREET: 411 Hackensack Ave, Continental Plaza, 4th</p> <p>Floor</p> <p>CITY: Hackensack</p> <p>STATE: New Jersey</p> <p>COUNTRY: USA</p> <p>ZIP: 07601</p> <p>COMPUTER READABLE FORM:</p> <p>MEDIUM TYPE: Floppy disk</p> <p>COMPUTER: IBM PC compatible</p> <p>OPERATING SYSTEM: PC-DOS/MS-DOS</p> <p>SOFTWARE: PatentIn Release #1.0, Version #1.30</p> <p>CURRENT APPLICATION DATA:</p> <p>APPLICATION NUMBER: US/09782,857A</p> <p>FILING DATE: 14-Feb-2001</p> <p>CLASSIFICATION: &lt;Unknown&gt;</p> <p>PRIOR APPLICATION DATA:</p> <p>APPLICATION NUMBER: 08/810,572</p> <p>FILING DATE: &lt;Unknown&gt;</p> <p>ATTORNEY/AGENT INFORMATION:</p> <p>NAME: Jackson Esq., David A.</p> <p>REGISTRATION NUMBER: 26,742</p> <p>REFERENCE/DOCKET NUMBER: 1340-1-007</p> <p>TELEPHONE: 201-487-5800</p> <p>TELEFAX: 201-343-1684</p> <p>INFORMATION FOR SEQ ID NO: 2:</p> <p>SEQUENCE CHARACTERISTICS:</p> <p>LENGTH: 293 amino acids</p> <p>TYPE: amino acid</p> <p>STRANDEDNESS: single</p> <p>TOPOLOGY: linear</p> <p>MOLECULE TYPE: protein</p> <p>HYPOTHETICAL: NO</p> <p>FRAGMENT TYPE: N-terminal</p> <p>ORIGINAL SOURCE:</p> <p>ORGANISM: Homo sapiens</p> <p>SEQUENCE DESCRIPTION: SEQ ID NO: 2:</p> <p>US-09-782-857A-2</p> <p>Query Match 100.0%; Score 315; DB 4; Length 293;</p> <p>Best Local Similarity 100.0%; Pred. No. 1.6e-33;</p> <p>Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>		
QY	1	ENKLRSPVNLPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db	105	ENKLRSPVNLPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
QY	61 ST 62	
Db	165 ST 166	
<p>RESULT 8</p> <p>US-09-879-919-22</p> <p>Sequence 22, Application US/09879919</p> <p>Patent No. 6541224</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Yu, Guo-Liang, et al.</p> <p>TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon</p> <p>FILE REFERENCE: PF253P1</p> <p>CURRENT APPLICATION NUMBER: US/09/879,919</p> <p>CURRENT FILING DATE: 2001-06-14</p> <p>PRIOR APPLICATION NUMBER: 60/293,499</p> <p>PRIOR FILING DATE: 2001-05-25</p> <p>PRIOR APPLICATION NUMBER: 60/277,978</p> <p>PRIOR FILING DATE: 2001-03-23</p> <p>PRIOR APPLICATION NUMBER: 60/276,248</p> <p>PRIOR FILING DATE: 2001-03-16</p> <p>PRIOR APPLICATION NUMBER: 60/254,875</p> <p>PRIOR FILING DATE: 2000-12-13</p> <p>PRIOR APPLICATION NUMBER: 60/241,952</p> <p>PRIOR FILING DATE: 2000-10-23</p> <p>PRIOR APPLICATION NUMBER: 60/211,537</p> <p>PRIOR FILING DATE: 2000-06-15</p> <p>PRIOR APPLICATION NUMBER: 08/815,783</p> <p>PRIOR FILING DATE: 1997-03-12</p> <p>PRIOR APPLICATION NUMBER: 60/016,812</p> <p>PRIOR FILING DATE: 1996-03-14</p> <p>NUMBER OF SEQ ID NOS: 26</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 22</p> <p>LENGTH: 293</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-879-919-22</p> <p>Query Match 100.0%; Score 315; DB 4; Length 293;</p> <p>Best Local Similarity 100.0%; Pred. No. 1.6e-33;</p> <p>Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>		
QY	1	ENKLRSPVNLPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db	105	ENKLRSPVNLPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
QY	61 ST 62	
Db	165 ST 166	
<p>RESULT 9</p> <p>US-09-848-295-4</p> <p>Sequence 4, Application US/09848295</p> <p>Patent No. 6623941</p> <p>GENERAL INFORMATION:</p> <p>APPLICANT: Baker, Kevin</p> <p>APPLICANT: Ruben, Steven M.</p> <p>TITLE OF INVENTION: Human Tumor Necrosis Factor TR20 and Methods Based</p> <p>FILE REFERENCE: PF527</p> <p>CURRENT APPLICATION NUMBER: US/09/848,295</p> <p>CURRENT FILING DATE: 2001-05-04</p> <p>PRIOR APPLICATION NUMBER: 60/202,193</p> <p>PRIOR FILING DATE: 2000-05-05</p> <p>NUMBER OF SEQ ID NOS: 4</p> <p>SOFTWARE: PatentIn Ver. 2.1</p> <p>SEQ ID NO 4</p> <p>LENGTH: 293</p> <p>TYPE: PRT</p> <p>ORGANISM: Homo sapiens</p> <p>US-09-848-295-4</p> <p>Query Match 100.0%; Score 315; DB 4; Length 293;</p> <p>Best Local Similarity 100.0%; Pred. No. 1.6e-33;</p> <p>Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>		
QY	1	ENKLRSPVNLPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db	105	ENKLRSPVNLPELRRQSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
QY	61 ST 62	
Db	165 ST 166	

Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
Qy 61 ST 62  
Db 165 ST 166

RESULT 10  
US-09-854-864-14  
; Sequence 14, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-14

Query Match 100.0%; Score 315; DB 4; Length 293;  
Best Local Similarity 100.0%; Pred. No. 1.6e-33; Mismatches 0; Indels 0; Gaps 0;  
Matches 62; Conservative 0;  
Qy 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
Qy 61 ST 62  
Db 165 ST 166

RESULT 11  
US-09-854-864-18  
; Sequence 18, Application US/09854864  
; Patent No. 6774106  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; TITLE OF INVENTION: BLYS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 18  
; LENGTH: 397  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-18

Query Match 98.4%; Score 310; DB 4; Length 397;  
Best Local Similarity 100.0%; Pred. No. 1.1e-32; Mismatches 0; Indels 0; Gaps 0;  
Matches 61; Conservative 0;  
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Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRSEASPALPGLKLSADQVALVY 164  
Qy 61 S 61  
Db 165 S 165

RESULT 12  
US-09-252-991A-24431  
; Sequence 24431, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 24431  
; LENGTH: 428  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-24431

Query Match 21.0%; Score 66; DB 4; Length 428;  
Best Local Similarity 40.9%; Pred. No. 2.5; Mismatches 8; Indels 10; Gaps 2;  
Matches 18; Conservative 8;  
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Db 254 LAQQAGHROQH-----HEGLE-----EAPAPFDLLLAADQVA 287

RESULT 13  
US-09-252-991A-23205  
; Sequence 23205, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 23205  
; LENGTH: 328  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-23205

Query Match 20.3%; Score 64; DB 4; Length 328;  
Best Local Similarity 31.8%; Pred. No. 3.3; Mismatches 23; Indels 14; Gaps 3;  
Matches 21; Conservative 8;  
Qy 6 SPVN--LPPELRQSRGEVNNSDNSGRYQGL-----EHRGSEASPALPGLKLS 52  
Db 165 APVGAALPPAARRQRTGPA--GGHRDGRRTALGVFALRRRLDPDFPGFARPGLDGIEQA 223  
Qy 53 ADQVAL 58  
Db 224 AHRVAV 229



RESULT 14  
US-09-252-991A-18308  
; Sequence 18308, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 18308  
; LENGTH: 341  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-18308

Query Match 20.3%; Score 64; DB 4; Length 341;  
Best Local Similarity 30.5%; Pred. No. 3.4;  
Matches 18; Conservative 7; Mismatches 20; Indels 14; Gaps 2;  
Qy 9 NLPELRR-----QRSGEVENNSDNGRYQGLEHRCSEASPALPGLKLSADQ 55  
Db 144 HLPFRRRAAARGFERPQTG--RHGPDRAHRRRPQHRTAVGPRLLPAATVERDQ 200

RESULT 15  
US-09-252-991A-30669  
; Sequence 30669, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30669  
; LENGTH: 179  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30669

Query Match 19.7%; Score 62; DB 4; Length 179;  
Best Local Similarity 41.3%; Pred. No. 2.7;  
Matches 19; Conservative 4; Mismatches 19; Indels 4; Gaps 2;  
Qy 10 LPPELRRQRSGEVENNSDNGRY--QGLEHRCSEASPALPGLKLSA 53  
Db 91 LHPQLRRQPAHHPGTTTERRRRCQDQGLRRPGSGAD--LPGLRSQA 134

Search completed: August 12, 2005, 15:15:35  
Job time : 23 secs

GenCore version 5.1.6  
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# QM protein - protein search, using sw model

Run on: August 12, 2005, 15:11:59 ; Search time 157 Seconds  
(without alignments)  
154.342 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_105\_166

Perfect score: 315  
Sequence: 1 ENKLSPVNLPELRRQSG.....SPALPGLKLSADQVALVYST 62

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Total number of hits satisfying chosen parameters: 1755696

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/2/pubaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/2/pubaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/2/pubaa/US06\_NEW\_PUB.pep.\*
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- 11: /cgn2\_6/ptodata/2/pubaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/2/pubaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/2/pubaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/2/pubaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/2/pubaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/2/pubaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/2/pubaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/2/pubaa/US10F\_PUBCOMB.pep.\*
- 19: /cgn2\_6/ptodata/2/pubaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/2/pubaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/2/pubaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/2/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	315	100.0	166	9	US-09-854-864-15
2	315	100.0	166	9	US-09-855-158-15
3	315	100.0	166	14	US-10-293-816-6
4	315	100.0	246	17	US-10-626-914-14
5	315	100.0	246	17	US-10-861-049-53
6	315	100.0	246	20	US-11-021-874-53
7	315	100.0	247	17	US-10-485-489-14
8	315	100.0	265	17	US-10-626-914-17
9	315	100.0	265	17	US-10-485-489-19
10	315	100.0	265	17	US-10-861-049-36
11	315	100.0	265	20	US-11-021-874-36

12	315	100.0	293	9	US-09-879-919-22	Sequence 22, Appl
13	315	100.0	293	9	US-09-854-864-14	Sequence 14, Appl
14	315	100.0	293	9	US-09-855-158-14	Sequence 14, Appl
15	315	100.0	293	9	US-09-961-376-2	Sequence 2, Appl
16	315	100.0	293	9	US-09-779-050A-42	Sequence 42, Appl
17	315	100.0	293	10	US-09-302-863-2	Sequence 2, Appl
18	315	100.0	293	10	US-09-855-564-2	Sequence 2, Appl
19	315	100.0	293	13	US-10-087-192-1650	Sequence 1650, Ap
20	315	100.0	293	13	US-10-084-971-2	Sequence 4, Appl
21	315	100.0	293	14	US-10-068-725-4	Sequence 46, Appl
22	315	100.0	293	14	US-10-151-882-46	Sequence 2, Appl
23	315	100.0	293	14	US-10-293-816-2	Sequence 8, Appl
24	315	100.0	293	14	US-10-008-063-8	Sequence 2, Appl
25	315	100.0	293	14	US-10-152-363A-2	Sequence 22, Appl
26	315	100.0	293	14	US-10-268-951-22	Sequence 1, Appl
27	315	100.0	293	15	US-10-258-368-1	Sequence 4, Appl
28	315	100.0	293	15	US-10-618-797-4	Sequence 7, Appl
29	315	100.0	293	16	US-10-742-634-7	Sequence 27, Appl
30	315	100.0	293	16	US-10-748-119-27	Sequence 4, Appl
31	315	100.0	293	17	US-10-684-149-4	Sequence 3, Appl
32	315	100.0	293	17	US-10-626-914-3	Sequence 3, Appl
33	315	100.0	293	17	US-10-485-489-3	Sequence 25, Appl
34	315	100.0	293	17	US-10-861-049-25	Sequence 25, Appl
35	315	100.0	293	20	US-11-021-874-25	Sequence 12, Appl
36	315	100.0	301	15	US-10-258-368-12	Sequence 18, Appl
37	310	98.4	397	9	US-09-854-864-18	Sequence 18, Appl
38	310	98.4	397	9	US-09-855-158-18	Sequence 43, Appl
39	300.5	95.4	291	9	US-09-779-050A-43	Sequence 15, Appl
40	287	91.1	404	15	US-10-258-368-15	Sequence 47, Appl
41	279.5	88.7	57	9	US-09-779-050A-47	Sequence 50, Appl
42	260	82.5	392	14	US-10-152-363A-50	Sequence 1647, Ap
43	141.5	44.9	249	13	US-10-087-192-1647	Sequence 56, Appl
44	85	27.0	357	14	US-10-152-363A-56	Sequence 181850,
45	68	21.6	305	15	US-10-424-599-181850	

## ALIGNMENTS

RESULT 1  
US-09-854-864-15  
; Sequence 15, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCWA,  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 15  
; LENGTH: 166  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-15

Query Match	100.0%	Score 315;	DB 9;	Length 166;
Best Local Similarity	100.0%	Pred. No. 1.7e-30;		
Matches	62;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;
Qy	1	ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY	60	
Db	105	ENKLSPVNLPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY	164	
Qy	61	ST 62		

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Db      165 ST 166

RESULT 2
US-09-855-158-15
; Sequence 15, Application US/09855158
; Publication No. US20020086018A1
; GENERAL INFORMATION:
; APPLICANT: THEILL, LARS EYDE
; APPLICANT: YU, GANG
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BL
; FILE REFERENCE: A-686A
; CURRENT APPLICATION NUMBER: US/09/855,158
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/214,591
; PRIOR FILING DATE: 2000-06-27
; PRIOR APPLICATION NUMBER: US 60/204,039
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-158-15

Query Match      100.0%; Score 315; DB 9; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db      105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
QY      61 ST 62
Db      165 ST 166

RESULT 3
US-10-293-816-6
; Sequence 6, Application US/10293816
; Publication No. US20030082173A1
; GENERAL INFORMATION:
; APPLICANT: Bram, Richard J.
; APPLICANT: Von Bulow, Gotz
; TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
; FILE REFERENCE: 44158/254623
; CURRENT APPLICATION NUMBER: US/10/293,816
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: US 09/782,857
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/290,333
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: US 08/810,572
; PRIOR FILING DATE: 1997-03-03
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-816-6

Query Match      100.0%; Score 315; DB 14; Length 166;
Best Local Similarity 100.0%; Pred. No. 1.7e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db      105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164
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QY      61 ST 62
Db      165 ST 166

RESULT 4
US-10-626-914-14
; Sequence 14, Application US/10626914
; Publication No. US20050043516A1
; GENERAL INFORMATION:
; Fatin Docket Preview
; APPLICANT: CHUNTHARAPAI, ANAN
; APPLICANT: GREWAL, IOBAL
; APPLICANT: KIM, KYUNG JIN
; APPLICANT: YAN, MINHONG
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof
; FILE REFERENCE: P1942R1
; CURRENT APPLICATION NUMBER: US/10/626,914
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 60/398,530
; PRIOR FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 14
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-626-914-14

Query Match      100.0%; Score 315; DB 17; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
Db      59 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 118
QY      61 ST 62
Db      119 ST 120

RESULT 5
US-10-861-049-53
; Sequence 53, Application US/10861049
; Publication No. US20050095243A1
; GENERAL INFORMATION:
; APPLICANT: Andrew Chan
; APPLICANT: Qian Gong
; APPLICANT: Flavius Martin
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS
; FILE REFERENCE: P2040R1US
; CURRENT APPLICATION NUMBER: US/10/861,049
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: US 60/476,531
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: US 60/476,481
; PRIOR FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: US 60/476,414
; PRIOR FILING DATE: 2003-06-05
; NUMBER OF SEQ ID NOS: 145
; SEQ ID NO 53
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-861-049-53

Query Match      100.0%; Score 315; DB 17; Length 246;
Best Local Similarity 100.0%; Pred. No. 2.8e-30;
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60
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Db 59 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 118

Qy 61 ST 62

119 ST 120

## RESULT 6

US-11-021-874-53  
; Sequence 53, Application US/11021874  
; Publication No. US20050163775A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; APPLICANT: Flavius Martin  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R1P1  
; CURRENT APPLICATION NUMBER: US/11/021,874  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/861,049  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 165  
; SEQ ID NO 53  
; LENGTH: 246  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-874-53

Query Match 100.0%; Score 315; DB 20; Length 246;  
Best Local Similarity 100.0%; Pred. No. 2.8e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 59 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 118

Qy 61 ST 62

119 ST 120

## RESULT 7

US-10-485-489-14  
; Sequence 14, Application US/10485489  
; Publication No. US20050070689A1  
; GENERAL INFORMATION:  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Grewal, Iqbal  
; APPLICANT: Ridgway, John  
; APPLICANT: Yan, Minhong  
; TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof  
; FILE REFERENCE: 11669.175USWO  
; CURRENT APPLICATION NUMBER: US/10/485,489  
; CURRENT FILING DATE: 2004-01-30  
; PRIOR APPLICATION NUMBER: PCT/US02/23487  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US 60/310,114  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/377,171  
; PRIOR FILING DATE: 2002-04-30  
; NUMBER OF SEQ ID NOS: 19  
; SEQ ID NO 14  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-489-14

Query Match 100.0%; Score 315; DB 17; Length 247;  
Best Local Similarity 100.0%; Pred. No. 2.8e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 59 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 118

Qy 61 ST 62

119 ST 120

## RESULT 8

US-10-626-914-17  
; Sequence 17, Application US/10626914  
; Publication No. US20050043516A1  
; GENERAL INFORMATION:  
; Patin Docket Preview  
; APPLICANT: CHUNTHARAPAI, ANAN  
; APPLICANT: GREWAL, IQBAL  
; APPLICANT: KIM, KYUNG JIN  
; APPLICANT: YAN, MINHONG  
; TITLE OF INVENTION: TACI Antibodies and Uses Thereof  
; FILE REFERENCE: P1942R1  
; CURRENT APPLICATION NUMBER: US/10/626,914  
; CURRENT FILING DATE: 2003-07-25  
; PRIOR APPLICATION NUMBER: US 60/398,530  
; PRIOR FILING DATE: 2002-07-25  
; NUMBER OF SEQ ID NOS: 17  
; SEQ ID NO 17  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-626-914-17

Query Match 100.0%; Score 315; DB 17; Length 265;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 60

Db 105 ENKLSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRSEASPALPGLKLSADQVALVY 164

Qy 61 ST 62

165 ST 166

## RESULT 9

US-10-485-489-19  
; Sequence 19, Application US/10485489  
; Publication No. US20050070689A1  
; GENERAL INFORMATION:  
; APPLICANT: Dixit, Vishva  
; APPLICANT: Grewal, Iqbal  
; APPLICANT: Ridgway, John  
; APPLICANT: Yan, Minhong  
; TITLE OF INVENTION: TACIS and BR3 Polypeptides and Uses Thereof  
; FILE REFERENCE: 11669.175USWO  
; CURRENT APPLICATION NUMBER: US/10/485,489  
; CURRENT FILING DATE: 2004-01-30  
; PRIOR APPLICATION NUMBER: PCT/US02/23487  
; PRIOR FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: US 60/310,114  
; PRIOR FILING DATE: 2001-08-03  
; PRIOR APPLICATION NUMBER: US 60/377,171  
; PRIOR FILING DATE: 2002-04-30  
; NUMBER OF SEQ ID NOS: 19  
; SEQ ID NO 19  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-485-489-19

## US-10-485-489-19

Query Match 100.0%; Score 315; DB 17; Length 265;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
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Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
|||||

QY 61 ST 62  
||  
Db 165 ST 166

## RESULT 10

US-10-861-049-36  
; Sequence 36, Application US/10861049  
; Publication No. US20050095243A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R1US  
; CURRENT APPLICATION NUMBER: US/10/861,049  
; CURRENT FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05  
; NUMBER OF SEQ ID NOS: 145  
; SEQ ID NO 36  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-861-049-36

Query Match 100.0%; Score 315; DB 17; Length 265;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
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Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
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QY 61 ST 62  
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Db 165 ST 166

## RESULT 11

US-11-021-874-36  
; Sequence 36, Application US/11021874  
; Publication No. US20050163775A1  
; GENERAL INFORMATION:  
; APPLICANT: Andrew Chan  
; APPLICANT: Qian Gong  
; TITLE OF INVENTION: COMBINATION THERAPY FOR B CELL DISORDERS  
; FILE REFERENCE: P2040R1P1  
; CURRENT APPLICATION NUMBER: US/11/021,874  
; CURRENT FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/861,049  
; PRIOR FILING DATE: 2004-06-04  
; PRIOR APPLICATION NUMBER: US 60/476,531  
; PRIOR FILING DATE: 2003-06-06  
; PRIOR APPLICATION NUMBER: US 60/476,481  
; PRIOR FILING DATE: 2003-06-05  
; PRIOR APPLICATION NUMBER: US 60/476,414  
; PRIOR FILING DATE: 2003-06-05

## ; NUMBER OF SEQ ID NOS: 165

; SEQ ID NO 36  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-021-874-36

Query Match 100.0%; Score 315; DB 20; Length 265;  
Best Local Similarity 100.0%; Pred. No. 3.1e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
|||||  
Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
|||||

QY 61 ST 62  
||  
Db 165 ST 166

## RESULT 12

US-09-879-919-22  
; Sequence 22, Application US/09879919  
; Patent No. US20020064829A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Guo-Liang, et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon  
; FILE REFERENCE: PF253P1  
; CURRENT APPLICATION NUMBER: US/09/879,919  
; CURRENT FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: 60/293,499  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: 60/277,978  
; PRIOR FILING DATE: 2001-03-23  
; PRIOR APPLICATION NUMBER: 60/276,248  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/254,875  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 60/241,952  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/211,537  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 08/815,783  
; PRIOR FILING DATE: 1997-03-12  
; PRIOR APPLICATION NUMBER: 60/016,812  
; PRIOR FILING DATE: 1996-03-14  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-879-919-22

Query Match 100.0%; Score 315; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.5e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
|||||  
Db 105 ENKLRSPVNLPPELRRQSRGEVNNSDNSGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
|||||

QY 61 ST 62  
||  
Db 165 ST 166

## RESULT 13

US-09-854-864-14  
; Sequence 14, Application US/09854864  
; Patent No. US20020081296A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE

; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA,  
; FILE OF INVENTION: ELIS/AGP-3, AND TACI  
; FILE REFERENCE: A-686B  
; CURRENT APPLICATION NUMBER: US/09/854,864  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-854-864-14

Query Match 100.0%; Score 315; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.5e-30; Indels 0; Gaps 0;  
Matches 62; Conservative 0; Mismatches 0

Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
Qy 61 ST 62  
Db 165 ST 166

## RESULT 14

US-09-855-158-14  
; Sequence 14, Application US/09855158  
; Publication No. US20020086018A1  
; GENERAL INFORMATION:  
; APPLICANT: THEILL, LARS EYDE  
; APPLICANT: YU, GANG  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF MATTER CONCERNING APRIL/G70, BCMA, BI  
; FILE OF INVENTION: 3, AND TACI  
; FILE REFERENCE: A-686A  
; CURRENT APPLICATION NUMBER: US/09/855,158  
; CURRENT FILING DATE: 2001-09-11  
; PRIOR APPLICATION NUMBER: US 60/214,591  
; PRIOR FILING DATE: 2000-06-27  
; PRIOR APPLICATION NUMBER: US 60/204,039  
; PRIOR FILING DATE: 2000-05-12  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-855-158-14

Query Match 100.0%; Score 315; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.5e-30;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
Qy 61 ST 62  
Db 165 ST 166

## RESULT 15

US-09-961-376-2  
; Sequence 2, Application US/09961376  
; Patent No. US20020106736A1  
; GENERAL INFORMATION:

; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor TR17  
; FILE REFERENCE: PF524P1  
; CURRENT APPLICATION NUMBER: US/09/961,376  
; CURRENT FILING DATE: 2001-09-25  
; PRIOR APPLICATION NUMBER: 60/254,874  
; PRIOR FILING DATE: 2000-12-13  
; PRIOR APPLICATION NUMBER: 60/235,991  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: 09/533,822  
; PRIOR FILING DATE: 2000-03-24  
; PRIOR APPLICATION NUMBER: 60/188,208  
; PRIOR FILING DATE: 2000-03-10  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 293  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-961-376-2

Query Match 100.0%; Score 315; DB 9; Length 293;  
Best Local Similarity 100.0%; Pred. No. 3.5e-30; Indels 0; Gaps 0;  
Matches 62; Conservative 0; Mismatches 0

Qy 1 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSPVNLPPELRRQSGEVENNSDNGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
Qy 61 ST 62  
Db 165 ST 166

Search completed: August 12, 2005, 15:26:34  
Job time : 158 secs

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C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S16356  
R;Mevel-Ninio, M.; Terracol, R.; Kafatos, F.C.  
EMBO J. 10, 2259-2266, 1991  
A;Title: The ovo gene of Drosophila encodes a zinc finger protein required for female germline development  
A;Reference number: S16356; MUID:91293102; PMID:1712294  
A;Accession: S16356  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-1213 <MEV>  
A;Cross-references: UNIPROT:Q8T8L9; EMBL:X59772  
C;Genetics:  
A;Gene: FlyBase:Ovo  
A;Cross-references: FlyBase:FBgn0003028  
A;Introns: 931/3; 1152/3

Query Match 19.4%; Score 61; DB 2; Length 1213;  
Best Local Similarity 36.1%; Pred.No. 57;  
Matches 13; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 10 LPPELRQRSGEVNNSDNGRYQGLEGHRGSEASPA 45  
||||| :||| :||| :||| :|||  
DB 384 LPPFYELKSGQQSTASNVTGQSPCANHSHFNANPA 419

RESULT 8  
T29518  
hypothetical protein T25F10.2 - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 09-Jul-2004  
C;Accession: T29518  
R;Pauley, A.; Gattung, S.  
submitted to the EMBL Data Library, July 1996  
A;Description: The sequence of C. elegans cosmid T25F10.  
A;Reference number: Z20634  
A;Accession: T29518  
A;Status: preliminary; translated from GB/EMBL/DDBB  
A;Molecule type: DNA  
A;Residues: 1-379 <PAU>  
A;Cross-references: UNIPROT:O02424; EMBL:U64856; PIDN:AAB04986.1; GSPDB:GN00023; CESP:T50  
A;Experimental source: strain Bristol N2; clone T25F10  
C;Genetics:  
A;Gene: CESP:T25F10.2  
A;Map position: 5  
A;Introns: 96/3; 129/3; 153/3; 250/3; 286/1; 324/3; 362/2  
C;Superfamily: inhibin

Query Match 19.2%; Score 60.5; DB 2; Length 379;  
Best Local Similarity 34.1%; Pred.No. 18;  
Matches 14; Conservative 9; Mismatches 17; Indels 1; Gaps 1;

QY 6 SPVNLPPELRQRSGEVNNSDNGRYQGLEGHRGSEASPAL 46  
:||| :||| :||| :||| :|||  
DB 224 SDLSEPSSVRKKQAQT-GNSERKNRKGRKHNTAEESNL 263

RESULT 9  
B84583  
hypothetical protein At2g19950 [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 09-Jul-2004  
C;Accession: B84583  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Unayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: B84583  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-713 <STO>  
A;Cross-references: UNIPROT:O8SAN9; GR:AR002093; NID:Q6598515; PIDN:AAPI8622.1; GSPDB:GN00023; CESP:

262 ELRNQASQSESS-----IDHTGKNTSPDNPGTNAEEDE 296

**RESULT 12**

A46216  
transcription factor Skn-1, splice form a - rat  
N/Alternate names: Skn-1a  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 19-Nov-1993 #sequence\_revision 18-Nov-1994 #text\_change 05-Dec-1997  
C/Accession: A46216  
P/Andersen, B.; Schonemann, M.D.; Flynn, S.E.; Pearce II, R.V.; Singh, H.; Rosenfeld, M.  
Science 260, 78-82, 1993  
A/Title: Skn-1a and Skn-1i: two functionally distinct Oct-2-related factors expressed in  
A/Reference number: A46216; MUID:93219836; PMID:7682011  
A/Accession: A46216  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-430 <AND>  
A/Cross-references: GB:L23962; NID:q393220  
A/Note: sequence extracted from NCBI backbone (NCBIP:128572)  
C/Superfamily: transcription factor Oct-2; homeobox homology; POU domain homology  
C/Keywords: alternative splicing; DNA binding; homeobox; nucleus; transcription regulati  
P:183-250/Domain: POU domain homology <POU>  
P:275-331/Domain: homeobox homology <HOX>

Query Match 18.7%; Score 59; DB 1; Length 430;  
Best Local Similarity 24.1%; Pred. No. 31;  
Matches 20; Conservative 11; Mismatches 20; Indels 32; Gaps 3;

Qy	8	VNLPEL-----RRQSGEVENNSDNG-----RYQGLEHR	38
		:  :  :	
		:  :  :	
Db	2	VNLEPWLSETKVSGDVADSTARSTFGVESGNDNRGLDFNRQIKTEDIGDTHESLSHR	61

QY 39 G---SEASPALPGLKLSADQVAL 58

db 62 PCHLTEGPTMPPGNOMSGDMSL 84

RESULT 13

Catalase (EC 1.11.1.6) precursor - fission yeast (*Schizosaccharomyces pombe*)  
 C:Species: Schizosaccharomyces pombe  
 C>Date: 27-Sep-1995 #sequence revision 27-Oct-1995 #text\_change 09-Jul-2004  
 C:Accession: JG4164; PC4041; T41598  
 R:Nakagawa, C.W.; Mutoh, N.; Hayashi, Y.  
 J. Biochem. 118, 109-116, 1995  
 A:Title: Transcriptional regulation of catalase gene in the fission yeast *Schizosaccharomyces pombe*  
 A:Reference number: JG4164; MUID:96015157; PMID:8537298  
 A:Accession: JG4164  
 A:Molecule type: DNA  
 A:Residues: 1-512 <NAK>  
 A:Cross-references: UNIPROT:P55306; GB:D55675; NID:G1905773; PIDN:BAA09526.1; PID:G87197  
 A:Accession: PC4041  
 A:Molecule type: protein  
 A:Residues: 277-286; 421-431 <NA2>  
 R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Bothe, G.; Pohl, T.  
 submitted to the EMBL Data Library, October 1998  
 A:Reference number: 222003  
 A:Accession: T41598  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-512 <LYN>  
 A:Cross-references: EMBL:AL031825; PIDN:CAA21232.1; GSPDB:GN00068; SPDB:SPCC757.07C  
 A:Experimental source: strain 372h-; cosmid C757  
 C:Comment: This enzyme is induced 8-fold in response to low concentrations of hydrogen H<sub>2</sub>  
 C:Genetics:  
 A:Gene: ctal; SPDB:SPCC757.07C  
 A:Map position: 3  
 C:Superfamily: catalase  
 C:Keywords: chromoprotein; heme; iron; metalloprotein; oxidoreductase  
 F:1-27/Domain: signal sequence #status predicted <SIG>  
 F:28-512/Product: catalase #status predicted <NAT>  
 F:60\_99\_133/Active site: His, Ser, Asn #status predicted

F:344/Binding site: heme iron (Tyr) (axial ligand) #status predicted

Query Match 18.7%; Score 59; DB 2; Length 512;  
Best Local Similarity 32.6%; Pred. No. 37;

QY 17 QRSGEVENNSDNGRYQGLEHRSSEAPLPGCLKLSADQVALV 59  
||| | : : | : : : : :  
Db 297 ORVGRETLNONPTNFFADIEQAGFSPSHMVPGEIVSADPVLQV 339

RESULT 14

T42369  
catalase [EC 1.11.1.6] - fission yeast (*Schizosaccharomyces pombe*) (fragment)  
C/Species: *Schizosaccharomyces pombe*  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 21-Jul-2000  
C/Accession: T42369  
R/Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.  
DNA Res. 4, 363-369, 1997  
A/Title: Identification of open reading frames in *Schizosaccharomyces pombe* cDNAs.  
A/Reference number: Z17323; MUID:98162722; PMID:9501991  
A/Accession: T42369  
A/Status: preliminary; translated from GB/EMBL/DBDJ  
A/Molecule type: mRNA  
A/Residues: 1-532 <YOS>  
A/Cross-references: EMBL:D891126; NID:g1749459; PIDN:BAAL3788.1; PID:g1749460  
A/Experimental source: strain PR745

Query Match 18.7%; Score 59; DB 2; Length 532;  
Best Local Similarity 32.6%; Pred. NO. 39;  
Matches 14; Conservative 8; Mismatches 21; Indels

**Qy**      17 QRSGEVENSNDNGRYQGLEHRGSEASPALGLKLSADQVALV 59  
||| : : : ||| : : : ||| : : : |||  
**Dd**      317 QRVRFTLQNPTNFFADIEOAGFSPSHMVPGEIUSADPVLQV 359

RESULT 15

T10696  
legumin-like protein 1 - common buckwheat  
C:Species: Fagopyrum esculentum (Common buckwheat)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 09-Jul-2004  
C:Accession: T10696  
R:Fujino, K.; Funatsuiki, H.; Inada, M.; Shimono, Y.; Kikuta, Y.  
submitted to the EMBL Data Library, September 1996  
A:Description: Expression and sequence analysis of cDNAs corresponding to genes differentially expressed in developing seeds of common buckwheat  
A:Reference number: Z17081  
A:Accession: T10696  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-565 <FUJ>  
A:Cross-references: UNIPROT:O33878; EMBL:D87980  
A:Experimental source: cv. Kitayuki; immature seed; 14 days after anthesis  
C:Superfamily: glycinin  
C:Keywords: seed; storage protein

Query Match 18.7%; Score 59; DB 2; Length 565;  
Best Local Similarity 28.2%; Pred. No. 42;  
Matches 24. Conservative 6; Mismatches 23; Indels

3 KI.RSPVNT.PPELRPRORSGEVENNSDNSGRYOGLE-----HRGSEAS----- 43

350 KT.RVPEEVEEELOREG---DRKRGSGRNGLEOAFCNLKEKONVNRPSRADVFENPRAG 406

44 -----PAI.PGI.KI.SADOVAL 58

db 407 RINTVNSNNLPILLEPTIOLSAOHVWL 431

Search completed: August 12, 2005, 15:12:18  
Job time : 24 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 12, 2005, 15:05:54 ; Search time 167 Seconds

(without alignments)  
190.113 Million cell updates/sec

Title: US-10-068-725-4\_COPY\_105\_166

Perfect score: 315

Sequence: 1 ENKLSPVNLPPELRRQSG.....SPALPGLKLSADQVALVYST 62

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 40 summaries

Database :

UniProt 03:\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	315	100.0	247	2 Q7Z6F5	Q7Z6F5 homo sapien
2	315	100.0	293	1 T13X HUMAN	O14836 homo sapien
3	141.5	44.9	249	1 T13X_MOUSE	Q9et35 mus musculus
4	140	44.4	156	2 Q9N146	Q9N146 macaca mula
5	84.5	26.8	702	2 Q9VH96	Q9VH96 drosophila
6	66	21.0	480	2 Q7YT18	Q7YT18 strongyloce
7	66	21.0	480	2 Q9GUY6	Q9GUY6 hemientrot
8	66	21.0	497	2 Q942X2	Q942X2 oryza sativ
9	66	21.0	509	2 Q98KE4	Q98KE4 rhizobium l
10	66	21.0	546	2 Q7VBZ9	Q7VBZ9 prochloroco
11	66	21.0	554	2 Q9JHT9	Q9JHT9 mus musculus
12	66	21.0	620	2 Q923H2	Q923H2 mus musculus
13	66	21.0	710	2 Q8CHT1	Q8CHT1 mus musculus
14	65.5	20.8	677	2 Q8TEJ7	Q8TEJ7 homo sapien
15	65	20.6	835	2 Q8KRE4	Q8KRE4 agrobacteri
16	64.5	20.5	87	2 Q9AY96	Q9AY96 ictalurus p
17	64.5	20.5	358	2 Q96BE7	Q96BE7 homo sapien
18	64	20.3	433	2 Q7XK69	Q7XK69 oryza sativ
19	63.5	20.2	800	2 Q6BJB7	Q6BJB7 debaryomyce
20	63.5	20.2	1665	2 Q8F1Z5	Q8F1Z5 candida gla
21	63	20.0	3374	2 Q8JUZ3	Q8JUZ3 montana myo
22	62.5	19.8	315	2 Q7J3U36	Q7J3U36 mycobacteri
23	62.5	19.8	1092	2 Q7KVZ8	Q7KVZ8 drosophila
24	62.5	19.8	1108	2 Q8MRI2	Q8MRI2 drosophila
25	62.5	19.8	1741	2 Q46095	Q46095 drosophila
26	62.5	19.8	1741	2 Q9W517	Q9W517 drosophila
27	62.5	19.8	1768	2 Q24153	Q24153 drosophila
28	62.5	19.8	6858	2 Q7QUW1	Q7QUW1 giardia lam
29	62	19.7	824	1 ROU HUMAN	Q00839 homo sapien
30	61.5	19.5	250	2 Q45690	Q45690 caenorhabdi
31	61.5	19.5	322	2 Q8PY32	Q8PY32 methanosarc

32 61.5 19.5 386 2 Q8FW75 Q8fw75 bruceella su  
33 61.5 19.5 470 2 Q8YC51 Q8yc51 bruceella me  
34 61.5 19.5 556 2 Q893U0 Q893u0 clostridium  
35 61 19.4 349 2 Q8N414 Q8n414 homo sapien  
36 61 19.4 349 2 Q8TCZ4 Q8tcz4 homo sapien  
37 61 19.4 399 2 Q9KXZ6 Q9kxz6 oligotropha  
38 61 19.4 453 2 Q9N6M8 Q9n6m8 drosophila  
39 61 19.4 453 2 Q9NGF6 Q9ngf6 drosophila  
40 61 19.4 453 2 Q9NGF7 Q9ngf7 drosophila  
41 61 19.4 578 2 Q8MSV2 Q8msv2 drosophila  
42 61 19.4 667 2 Q9DBU5 Q9dbu5 mus musculu  
43 61 19.4 975 2 Q9W4F1 Q9w4f1 drosophila  
44 61 19.4 1028 1 OVO DROME F51521 drosophila  
45 61 19.4 1222 2 Q8T8L9 Q8t8l9 drosophila

#### ALIGNMENTS

##### RESULT 1

Q7Z6F5 PRELIMINARY; PRT; 247 AA.  
AC Q7Z6F5  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Transmembrane activator and CAML interactor.  
GN Name=TNFRSF13B;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Zhou G., Ke R., Li H., Zheng G., Shen C., Lin L., Yang S.;  
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY302137; AAP57629.1; -;  
DR GO; GO:0016021; C:integral to membrane; IEA.  
KW Transmembrane.  
SQ SEQUENCE 247 AA; 26664 MW; 850E1F4C2578E8E6 CRC64;

Query Match 100.0%; Score 315; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. NO. 7.5e-29;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ENKLSPVNLPPELRRQSGEVNNSDGRYQGLEHRSSEASPALPGLKLSADQVALVY 60  
|||  
Db 59 ENKLSPVNLPPELRRQSGEVNNSDGRYQGLEHRSSEASPALPGLKLSADQVALVY 118  
|||

Qy 61 ST 62

Db 119 ST 120

##### RESULT 2

T13X HUMAN STANDARD; PRT; 293 AA.  
ID T13X HUMAN  
AC O14836;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).  
GN Name=TNFRSF13B; Synonyms=TACI;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=B-cell;  
RX MEDLINE=97458245; PubMed=9311921; DOI=10.1126/science.278.5335.138; von Buelow G.-U., Bram R.J.;



RT "NF-AT activation induced by a CAML-interacting member of the tumor  
RT necrosis factor receptor superfamily.";  
RL Science 278:138-141(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Blood;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Schetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toehiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Guntaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP FUNCTION.  
RX MEDLINE=20519647; PubMed=10956646; DOI=10.1074/jbc.M005224200;  
RA Wu Y., Bressette D., Carrell J.A., Kaufman T., Feng P., Taylor K.,  
RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., LaFleur D.,  
RA Migone T.S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,  
RA Olsen H.S., Kanakaraj P., Moore P.A., Baker K.P.;  
RT "Tumor necrosis factor (TNF) receptor superfamily member TACI is a  
RT high affinity receptor for TNF family members APRIL and BlyS.";  
RL J. Biol. Chem. 275:35478-35485(2000).  
RN [4]  
RP FUNCTION.  
RX MEDLINE=21170294; PubMed=10973284; DOI=10.1038/79802;  
RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,  
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,  
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;  
RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating  
RT humoral immunity.";  
RL Nat. Immunol. 1:252-256(2000).  
RN [5]  
RP INTERACTIONS WITH TRAF2 AND TRAF5.  
RX MEDLINE=20341628; PubMed=10880535;  
RA Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M.,  
RA Theill L.E., Colombero A., Solovyev I., Lee F., McCabe S., Elliott R.,  
RA Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Delaney J.,  
RA Meng S.Y., Boyle W.J., Hsu H.;  
RT "TACI is a TRAF-interacting receptor for TALL-1, a tumor necrosis  
RT factor family member involved in B cell regulation.";  
RL J. Exp. Med. 192:137-143(2000).  
RN [6]  
RP FUNCTION. Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS  
CC that binds both ligands with similar high affinity. Mediates  
CC calcineurin-dependent activation of NF-AT, as well as activation  
CC of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-  
CC cell function and the regulation of humoral immunity.  
CC -1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal  
CC domain of CAMLG with its C-terminus.  
CC -1- SUBCELLULAR LOCATION: Type III membrane protein.  
CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small  
CC intestine and peripheral blood leukocytes. Expressed in resting B-  
CC cells and activated T-cells, but not in resting T-cells.  
CC -1- SIMILARITY: Contains 2 TNFR-Cys repeats.  
CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.  
CC  
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CC -----  
DR EMBL; AF023614; AAC51790.1; -;  
DR EMBL; BC028072; AAH28072.1; -;  
DR HSSP; O9Y275; 1OOD.  
DR Genew; HGNC:18153; TNFRSF13B.  
DR MIM; 604907; -;  
DR GO; GO:0005887; C: integral to plasma membrane; TAS.  
DR GO; GO:0004872; F: receptor activity; TAS.  
DR GO; GO:0007166; P: cell surface receptor linked signal transdu. . .; TAS.  
DR InterPro; IPR001368; TNFR\_2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; FALSE\_NEG.  
KW Glycoprotein; Immune response; Receptor; Repeat; Signal-anchor;  
KW Transmembrane.  
FT DOMAIN 1 165 Extracellular (Potential).  
FT TRANSMEM 166 186 Signal-anchor for type III membrane  
FT FT 187 293 Cytoplasmic (Potential).  
FT REPEAT 33 67 TNFR-Cys 1.  
FT DISULFID 34 47 By similarity.  
FT DISULFID 50 62 By similarity.  
FT DISULFID 54 66 By similarity.  
FT DISULFID 71 86 By similarity.  
FT DISULFID 89 100 By similarity.  
FT DISULFID 93 104 By similarity.  
FT CARBOHYD 128 128 N-linked (GlcNAc. . .) (Potential).  
FT CONFLICT 251 251 P -> L (in Ref. 2).  
SQ SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;  
  
Query Match 100.0%; Score 315; DB 1; Length 293;  
Best Local Similarity 100.0%; Pred. No. 9.3e-29;  
Matches 62; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 ENKLRSPVNLPPELRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 60  
Db 105 ENKLRSPVNLPPELRQRSGEVENNSDGRYQGLEHGRGSEASPALPGLKLSADQVALVY 164  
  
QY 61 ST 62  
Db 165 ST 166  
  
RESULT 3  
TI3X MOUSE  
ID TI3X MOUSE STANDARD; PRT; 249 AA.  
AC Q9ET35; Q9DBZ3;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane  
DE activator and CAML interactor).  
GN Name=TNFRsf13b; Synonyms=Taci;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
ON NCBI\_TaxID=10990;  
RX [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen.  
RX MEDLINE=21177754; PubMed=10881172; DOI=10.1038/76889;  
RA Yan M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;  
RT "Identification of a receptor for BlyS demonstrates a crucial role in  
RT humoral immunity.";  
RL Nat. Immunol. 1:37-41(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Lung;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;

Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S., Nikafo I., Oeato N., Saico R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schrim L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Brad D., Brusic V., Chothia C., Corbani L.B., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Giasi C., Godzik A., Gough J., Grimond S., Guatinchich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lennhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Perlee G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Sempie C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C., Wu Ming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N., Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Havaehizaki Y.

"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."

Nature 420:563-573 (2002).

[3]

FUNCTION.

MEDLINE=20341628; PubMed=10880535;

Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M., Theill L.B., Colombero A., Solovjev I., Lee F., McCabe S., Elliott R., Miner K., Hawkins N., Guo J., Stolina M., Yu G., Wang J., Bellant J., Meng S.-Y., Boyle W.J., Hsu H.

"TACI is a TRAP-interacting receptor for TALL-1, a tumor necrosis factor family member involved in B cell regulation."

J. Exp. Med. 192:137-143 (2000).

[4]

FUNCTION.

MEDLINE=21322748; PubMed=11429548; DOI=10.1038/89782;

Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tumas D., Yan M., Dixit V.M., Ashkenazi A., Grewal I.S.

"TACI-ligand interactions are required for T cell activation and collagen-induced arthritis in mice."

Nat. Immunol. 2:632-637 (2001).

-1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAPF/BLYS that binds both ligands with similar high affinity. Mediates calcineurin-dependent activation of NF-AT, as well as activation of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-cell function and the regulation of humoral immunity (By similarity).

-1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal domain of CAMLW with its C-terminus (By similarity).

-1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

-1- SIMILARITY: Contains 2 TNFR-Cys repeats.

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EMBL; AF257673; AAC00081.1; --

EMBL; AK004668; BAB23457.1; --

MGD; MGI:1889411; Tnfrsf13b.

DR GO; GO:0005887; C: integral to plasma membrane; IDA.

DR GO; GO:0005031; F: tumor necrosis factor receptor activity; IDA.

DR InterPro; IPR001368; TNFR\_c6.

DR PROSITE; PS00652; TNFR\_NGFR\_1; FALSE\_NEG.

DR PROSITE; PS00505; TNFR\_NGFR\_2; FALSE\_NEG.

KW Immune response; Receptor; Repeat; Signal-anchor; Transmembrane.

FT DOMAIN 1 128 Extracellular (Potential).

FT TRANSMEM 129 149 Signal-anchor for type III membrane protein (Potential).

FT DOMAIN 150 249 Cytoplasmic (Potential).

FT REPEAT 5 38 TNFR-Cys 1.

FT REPEAT 42 76 TNFR-Cys 2.

FT DISULFID 6 19 By similarity.

FT DISULFID 22 34 By similarity.

FT DISULFID 26 38 By similarity.

FT DISULFID 43 58 By similarity.

FT DISULFID 61 72 By similarity.

FT DISULFID 65 76 By similarity.

FT CONFLICT 137 137 I -> F (in Ref. 2).

SQ SEQUENCE 249 AA; CB2F2D61C2931D81 CRC64;

Query Match 44.9%; Score 141.5; DB 1; Length 249;

Best Local Similarity 53.2%; Pred. No. 2.2e-08;

Matches 33; Conservative 7; Mismatches 13; Indels 9; Gaps 2;

QY 1 ENKLRSPVNLPPELRRQRSGEVNNDNSGRVYQGLEHGRGSEASPGLKLSADQVALVY 60

Db 77 EKPRSQANLQPELGRPQAGEVVRSDNSGRHQSGE-----PGLRLSSDQLTL-Y 127

QY 61 ST 62

Db 128 CT 129

RESULT 4

Q9N146 PRELIMINARY; PRT; 156 AA.

ID Q9N146

AC Q9N146

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)

DE Transmembrane activator (Fragment).

GN Name=NF-AT;

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Macaca.

OC Cercopithecoidea; Macaca.

OX NCBI\_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RA Arredondo J.

RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF272558; AAF73400.1; --

DR GO; GO:0016021; C: integral to membrane; IEA.

KW Transmembrane.

FT NON TER 1 1

SQ SEQUENCE 156 AA; 16170 MW; 8AD74E4D17D511D0 CRC64;

Query Match 44.4%; Score 140; DB 2; Length 156;

Best Local Similarity 96.6%; Pred. No. 1.8e-08;

Matches 28; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 34 GLEHGRGSEASPGLKLSADQVALVYST 62

Db 1 GLEHGRGSEASPGLKLSADQVALVYST 29

RESULT 5

Q9VH96 PRELIMINARY; PRT; 702 AA.

ID Q9VH96

AC Q9VH96

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE CG8358-PA (GH26575p).

GN ORFNames=CG8358;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 NCBI\_TaxID=7227;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Anantides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.H., Blazer J.H., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
 RA Abril J.P., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Berens P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foeller C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,  
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,  
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,  
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen T.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,  
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*";  
 Science 287:2185-2195(2000).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22426065; PubMed=12537568;  
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Javerty T., Muzny D.M., Nelson C.R.,  
 RA Pacle J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
 melanogaster euchromatic genome sequence";  
 Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22426070; PubMed=12537573;  
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celniker S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 a genomics perspective";  
 Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=22426069; PubMed=12537572;  
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradscky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,  
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 systematic review";  
 Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RP FlyBase;  
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RP FlyBase;  
 RN Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Berkley;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,  
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,  
 RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,  
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AE003683; AAF54423.1; -;  
 DR FLYBase; AY069219; AAL39364.1; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0008237; F:metallopeptidase activity; IEA.  
 DR GO; GO:0004243; F:neprilysin activity; IEA.  
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.  
 DR InterPro; IPR000718; Peptidase M13.  
 DR InterPro; IPR008753; Peptidase M13 N.  
 DR InterPro; IPR006025; Pept. M\_Zn\_BS.  
 DR Pfam; PF01431; Peptidase\_M13; 1.  
 DR Pfam; PF05649; Peptidase\_M13\_N; 1.  
 DR PRINTS; PS00786; NEPRILYSIN.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 KW Hydrolase; Metalloprotease; Protease; Zinc.  
 SQ SEQUENCE 702 AA; 80825 MW; 4F4CA1A39F1F0BB6 CRC64;  
 Query Match 26.8%; Score 84.5; DB 2; Length 702;  
 Best Local Similarity 40.0%; Pred. No. 0.4;  
 Matches 24; Conservative 9; Mismatches 12; Indels 15; Gaps 3;  
 QY 12 PELRRQRSGEV---ENNSDMSG-----RYQGLEHGRSE-ASPALPGLKLSADQV 56  
 DB 578 PEISRVNGKTTLDENIADNSGLRQALTAYRSHRQQLLEHPQERISDAMPGLDLTPQL 637  
 RESULT 6  
 Q7YT18  
 ID Q7YT18 PRELIMINARY; PRT; 480 AA.  
 AC Q7YT18  
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Lim homeodomain transcription factor 1.  
 OS Strongylocentrotus purpuratus (Purple sea urchin).  
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;  
 OC Strongylocentrotus.  
 OX NCBI\_TaxID=7668;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Oral ectoderm;  
 RC Oliveri P., Davidson E.H.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).  
 CC -!- SIMILARITY: Contains 2 LIM zinc-binding domains.  
 DR EMBL; AY339649; RAQ01662.1; -;  
 DR HSSP; P06601; 1FUJ.  
 DR GO; GO:0005634; C:Nucleus; IEA.  
 DR GO; GO:0003700; F:transcription factor activity; IEA.

DR PROSITE; PS00027; HOMEBOX\_1; 1.  
DR PROSITE; PS0071; HOMEBOX\_2; 1.  
DR PROSITE; PS00478; LIM DOMAIN\_1; 2.  
DR PROSITE; PS0023; LIM DOMAIN\_2; 2.  
KW DNA-binding; Homeobox; LIM domain; Metal-binding; Nuclear protein;  
KW Zinc.  
SQ SEQUENCE 480 AA; 53636 MW; EDCBCCBEC841A5D6 CRC64;

Query Match 21.0%; Score 66; DB 2; Length 480;  
Best Local Similarity 30.4%; Pred. No. 38;  
Matches 14; Conservative 10; Mismatches 18; Indels 4; Gaps 1;

QY 6 SPVNLPPELRRQRSGEV-----ENNSDNSGRYQGLEHRSSEASPALP 47  
DB 181 TTATTPDDLDLRVKDASIMNNNNNNNNNHNHEAGLENRENTAGIP 226

RESULT 8  
Q942X2 PRELIMINARY; PRT; 497 AA.

ID Q942X2 AC Q942X2; DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative serine/threonine kinase PBS1 protein.  
DE Names:P0492GG09.25;  
GN Oryza sativa (japonica cultivar-group).  
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=39947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=12447438; DOI=10.1038/nature01184;  
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,  
Ra Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,  
Ra Hosokawa S., Masutaka M., Arikawa K., Chiden Y., Hayaashi M.,  
Ra Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,  
Ra Hijishita S., Honda M., Ichikawa Y., Idonuma A., Ifijima M., Ikeda M.,  
Ra Ikano M., Itoh S., Itoh T., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,  
Ra Karasawa W., Katagiri S., Kituta A., Kobayashi N., Kono I.,  
Ra Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,  
Ra Nagaaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,  
Ra Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K, Shibata M.,  
Ra Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Teuji K.,  
Ra Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,  
Ra Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,  
Ra Yano M., Jiang J., Gojobori T.;  
RT "The genome sequence and structure of rice chromosome 1.";  
RL Nature 420:312-316(2002).  
RC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AP003266; BAB64203.1; -.  
DR Gramene; Q942X2; -.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004574; P:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPRO11009; Kinase like.  
DR InterPro; IPRO00719; Prot kinase.  
DR InterPro; IPRO08271; Ser thr\_pkin\_AS.  
DR ProDom; PD000001; Prot kinase; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 497 AA; 54925 MW; 6DB0C1FAPFE0213E CRC64;

Query Match 21.0%; Score 66; DB 2; Length 497;  
Best Local Similarity 35.9%; Pred. No. 40;  
Matches 23; Conservative 11; Mismatches 20; Indels 10; Gaps 4;

QY 4 LRSPVNLPPELRQQ--RGSEVE----NNSDNSGRYQGLEGH---RGSE-ASPALPGLKLSA 53  
DB 401 VRSPNHPSPLDLRPEARSSRAEVRTSTGDSGRSRLDLDLTGTGSQNGSPAQTGRKET 460

QY 54 DOVA 57  
DB 461 PR7A 464

RESULT 9  
Q98KE4 PRELIMINARY; PRT; 509 AA.  
AC Q98KE4  
DT 01-OCT-2001 (TrEMBLrel. 18, Created)  
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE T-imethylamine methyltransferase; MttB.  
GN OrderedLocusNames=ml1516;  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MAFF303099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.,  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT Mesorhizobium loti."  
RL DNA Res. 7:331-338(2000).  
DR GO: GO:0008168; F:methyltransferase activity; IEA.  
DR GO: GO:0016740; F:transferase activity; IEA.  
DR InterPro; IPR010426; MTTB.  
DR Pfam; PF06253; MTTB; 1.  
KW Complete proteome; Methyltransferase; Transferase.  
SQ SEQUENCE 509 AA; 54430 MW; 283A0E396332A2AC CRC64;

Query Match 21.0%; Score 66; DB 2; Length 509;  
Best Local Similarity 36.0%; Pred. No. 41;  
Matches 18; Conservative 7; Mismatches 19; Indels 6; Gaps 1;

QY 13 ELRRQSRGSEVNNDSGRYQGLEHGRGSEASPALGLKLSADQVALVYST 62  
DB 4 ERRGRGTGEAGSSRRPNVRSUK-----NPFLPQIFSDQDVASIHDT 47

RESULT 10  
Q7VBZ9 PRELIMINARY; PRT; 546 AA.  
AC Q7VBZ9  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE 3,4-dihydroxy-2-butanone 4-phosphate synthase.  
GN Name=ribB; OrderedLocusNames=Pro0943;  
OS Prochlorococcus marinus.  
OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=1219;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SARG / COMP 1375 / SS120;  
RX MEDLINE=22810154; PubMed=12917486; DOI=10.1073/pnas.1733211100;  
RA Dufréne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,  
RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,  
RA Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B.,  
RA Scanlan D.J., Tandeau de Marsac N., Weissbach J., Wincker P.,  
RA Wolf Y.I., Hess W.R.,  
RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,  
RT a nearly minimal oxypototrophic genome."  
RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025 (2003).

DR EMBL; AE017163; AAP99987.1; --.  
DR HSSP; Q8TG90; 1K49.  
DR GO: GO:0008686; F:3,4 dihydroxy-2-butanone-4-phosphate syntha. .; IEA.  
DR GO: GO:0003935; F:GTP cyclohydrolase II activity; IEA.  
DR GO: GO:0003231; P:Vitamin B2 biosynthesis; IEA.  
DR InterPro; IPR000422; DHP synthase.  
DR InterPro; IPR000926; GTP CyclohydroII.  
DR Pfam; PF00925; GTP Cyclohydro2; 1.  
DR Pfam; PF00034; DHP synthase; 1.  
DR TIGRfams; TIGR00505; r1bA; 1.  
DR TIGRfams; TIGR00506; ribB; 1.  
KW Complete proteome.  
SQ SEQUENCE 546 AA; 60348 MW; 05453CE83073B5FE CRC64;

Query Match 21.0%; Score 66; DB 2; Length 546;  
Best Local Similarity 27.9%; Pred. No. 45;  
Matches 17; Conservative 12; Mismatches 24; Indels 8; Gaps 1;

QY 5 RSPVNLPP-----ELRRQSRGSEVNNDSGRYQGLEHGRGSEASPALGLKLSADQV 56  
DB 382 REPLVNPDTYNANYLAIKRTKLGHVIGNDDSGKYVYIWKGIYSSNNLSAYKNKAQEI 441

QY 57 A 57  
DB 442 A 442

RESULT 11  
Q9JHT9 PRELIMINARY; PRT; 554 AA.  
AC Q9JHT9  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Guanine nucleotide exchange factor.  
GN Name=Ngef; Synonyms=gef;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20241931; PubMed=10777665; DOI=10.1006/geno.2000.6138;  
RA Rodrigues N.R., Theodosiou A.M., Nesbit M.A., Campbell L.,  
RA Tandle A.T., Saranath D., Davies K.E.,  
RT "Characterization of Ngef, a novel member of the Dbl family of genes  
RT expressed predominantly in the caudate nucleus."  
RL Genomics 65:53-61(2000).  
CC -1- SIMILARITY: Contains 1 PH domain.  
CC -1- SIMILARITY: Contains 1 SH3 domain.  
DR EMBL; AJ238898; CAC00698.1; --.  
DR HSSP; O08839; 1BB9.  
DR MGD; MGI:1858414; Ngef.  
DR GO: GO:0008151; P:cell growth and/or maintenance; IEA.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR011036; PH related.  
DR InterPro; IPR00219; RhGGEF.  
DR InterPro; IPR001452; SH3.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00621; RhGGEF; 1.  
DR Pfam; PF00018; SH3 1; 1.  
DR Pfam; PF00006; SH3; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00325; RhGGEF; 1.  
DR SMART; SM00326; SH3; 1.  
DR PROSITE; PS0010; DH 2; 1.  
DR PROSITE; PS00003; PH DOMAIN; 1.  
DR PROSITE; PS00002; SH3; 1.  
KW SH3 domain.  
SQ SEQUENCE 554 AA; 64837 MW; 5F3A8FAFBFF5914 CRC64;

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Query Match      21.0%; Score 66; DB 2; Length 554;
Best Local Similarity 32.1%; Pred. No. 45;
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;

QY 13 ELRRQRSGEVENNSDNS-----GRYQGLEHGRGSEASPALPGLKLSADQVALV 59
DB 34 ETRRQDAEIQGNSDGSQVGDAGEEBEEBEEBEEELASPPERRALPQICLL 86

RESULT 12
Q923H2          PRELIMINARY; PRT; 620 AA.
ID Q923H2
AC Q923H2
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ephexin.
GN Ephexin.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
MEDLINE=2134975; PubMed=11336673; DOI=10.1016/S0092-8674(01)00314-2;
RA Shamah S.M., Lin M.Z., Goldberg J.L., Estrach S., Sahin M., Hu L.,
RA Bazalakova M., Neve R., Corfas G., Debant A., Greenberg M.E.;
RT "Epha receptors regulate growth cone dynamics through the novel
RT guanine nucleotide exchange factor ephexin.";
RL Cell 105:233-244 (2001).
CC -1- SIMILARITY: Contains 1 PH domain.
CC EMBL; AY038025; AAK71494.1; -.
DR HSP; O08839; 1BB9.
DR MGD; MGI:1858414; Ngef.
DR GO; GO:0008151; P:cell growth and/or maintenance; IDA.
DR InterPro; IPR01036; PH-related.
DR InterPro; IPR000219; RhoGEF.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00010; DH 2; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 620 AA; 71445 MW; C2C3A9C1B6F78402 CRC64;

Query Match      21.0%; Score 66; DB 2; Length 620;
Best Local Similarity 32.1%; Pred. No. 52;
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;

QY 13 ELRRQRSGEVENNSDNS-----GRYQGLEHGRGSEASPALPGLKLSADQVALV 59
DB 100 ETRRQDAEIQGNSDGSQVGDAGEEBEEBEEBEEELASPPERRALPQICLL 152

RESULT 13
Q8CHT1          PRELIMINARY; PRT; 710 AA.
ID Q8CHT1
AC Q8CHT1
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ngef protein.
GN Ngef protein.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

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SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schenker C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toehiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinaki M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Matra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 PH domain.
CC EMBL; BC039279; AAK39279.1; -.
DR HSP; O08839; 1BB9.
DR MGD; MGI:1858414; Ngef.
DR GO; GO:0008151; P:cell growth and/or maintenance; IDA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR01036; PH-related.
DR InterPro; IPR000219; RhoGEF.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00621; RhoGEF; 1.
DR ProDom; PD000066; SH3; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00325; RhoGEF; 1.
DR SMART; SM00326; SH3; 1.
DR PROSITE; PS00010; DH 2; 1.
DR PROSITE; PS00003; PH DOMAIN; 1.
DR PROSITE; PS00002; SH3; 1.
KW SH3 domain.
SQ SEQUENCE 710 AA; 82198 MW; F255DE351E02A586 CRC64;

Query Match      21.0%; Score 66; DB 2; Length 710;
Best Local Similarity 32.1%; Pred. No. 61;
Matches 17; Conservative 8; Mismatches 22; Indels 6; Gaps 1;

QY 13 ELRRQRSGEVENNSDNS-----GRYQGLEHGRGSEASPALPGLKLSADQVALV 59
DB 190 ETRRQDAEIQGNSDGSQVGDAGEEBEEBEEBEEELASPPERRALPQICLL 242

RESULT 14
Q8TEJ7          PRELIMINARY; PRT; 677 AA.
ID Q8TEJ7
AC Q8TEJ7
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE FLJ00198 protein (Fragment).
GN Name=FLJ00198;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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